PCT-US98-16719-2.rsp

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Release 3.1 Copyright (نزن به 🖈
MPsrch_pp prote	protein - protein database search, using Smith-Waterman algorithm
Run on:	Fri Sep 25 13:10:22 1998; MasPar time 3.86 Seconds 435.183 Million cell updates/sec
Tabular output not generated	
itle: Description: Perfect Score: Sequence:	>PCT-US98-16719-2 (1-67) from PCTUS9816719A.pep 535 1 NSVHPCCDPVKCEPREGEHCDYCSGIIPDCPRNRYKGKED 67
Scoring table:	PAM 150 Gap 11
Searched:	69111 seqs, 25083644 residues
Post-processing:	Post-processing: Minimum Match O% Listing first 45 summaries
Database:	swiss-prot15 1:swiss1
Statistics:	Mean 34.560; Variance 52.485; scale 0.658

7.74e-48 7.92e-47 7.92e-47 4.63e-44 1.47e-43 1.47e-42 8.21e-42 8.21e-40 8.11e-40 8.11e-40 8.11e-40 8.11e-40 7.02e-35 7.02e-35 7.02e-35 7.02e-35 7.02e-35 7.02e-35 Š DESCRIPTION

DISINTEGRIN HALYSIN (P 7)

DISINTEGRIN TRIGRAMIN 4

DISINTEGRIN TRIGRAMIN 4

DISINTEGRIN TRIGRAMIN 4

DISINTEGRIN VIRIDIN (P 8)

DISINTEGRIN WOLDGSIN (2)

DISINTEGRIN MOLDGSIN (2)

DISINTEGRIN MOLDGSIN (4)

DISINTEGRIN BATILLIN (4)

DISINTEGRIN BATRACIN (4)

DISINTEGRIN JARARACIN (6)

DISINTEGRIN JARARACIN (6)

DISINTEGRIN TERRONAMIN (7)

DISINTEGRIN TERRONAMIN (7)

DISINTEGRIN GRANAMIN (7)

DISINTEGRIN BARBOURIN (7)

DISINTEGRIN BARBOURIN (7)

DISINTEGRIN BARBOURIN (7)

DISINTEGRIN BARBOURIN (7)

DISINTEGRIN ERISTICOPH (7) DISI_AGKHA
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DISI_CROVY
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DISI_CROVY
DISI_CROVY
DISI_ROTAT
DISI_ROTAT SUMMARIES 8 Length % Query Match 1 Score

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1.83e- 1.83e- 1.95e- 1.95e- 1.95e- 1.95e- 1.11e- 1.11e- 1.95e- 1.			÷		CEPTORS TO THE INHIBI	VENOM.		Gaps	IPF 71 : IRY 62		JR.) .
HEMORRHAGIC PROTEIN-RH HEMORRHAGIC METALLOPRO DISINTEGRIN BITAN (PLA DISINTEGRIN ELAVORIDIN DISINTEGRIN FLAVORIDIN DISINTEGRIN FLAVORIDIN CELL SURFACE ANTIGEN METALLO CELL SURFACE ANTIGEN METALLO METALLOTHIONEIN-II (MT METALLOTHIONEIN-I (MT NONSTRUCTURAL PROTEIN METALLOTHIONEIN (MT).		71 AA.	PDATE) UPDATE) TION ACTIVATION INHIBITOR ATA; TETRAPODA; REPTILIA;	TENG CM.;	EXACTION WITH PLATELET RECEPTORS A COMPLEX. ACT BY BINDING TO THE THE PLATELET SURFACE AND INHIBI BIN, PLATELET-ACTIVATING FACTOR	-IIIA PROTEIN FOUND IN SNAKE	ESION; VENOM. ARITY. ACHMENT SITE. CRC32;	; DB 1; Length 71; 7.74e-48; atches 16; Indels 0;	NPCCDAATCKLRQGAQCAEGLCCDQCRFMKKGTVCRIARGDDMDDYCNGISAGCPRN : : : : : HPCCDPVKCEPREGEHCISGPCCRNCYFLRAGTVCKRAVGDDVDDYCSGITPDCPRN	71 AA.	NCE UPDATE) MIDN UPDATE) SCREGATION ACTIVATION INHIBITOR S (EASTERN COTTONMOUTH).
DISR_AGKRH HRTE_CROAT DISI_BITAR DISS_TRIFL DISK_TRIFL DISK_TRIFL MSZ_MOUSE DISJ_BOTJA MRZ_HRIB_TRIFL MTZ_CALSI MTS_SCYSE MTZ_SCYSE MTZ_SCYSE MTZ_SCYSE WF_UMAN VV_PI4HB VV_PI4HB MTZ_SCYSE RPCI_GIALA MTZ_SCYSE RPCI_GIALA MTZ_SCYSE	ALIGNMENTS	PRT;	01-MAY-1991 (REL. 18, CREATED) 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE) 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE) DISINTEGRIN HALYSIN (PLATELET AGGREGATION ACT AGKIGTRODON HALYS BLOMHOFFI (MAMUSHI). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET LEPIDOSAURIA; SERPENTES.	YANG C.H.,	RINGEN INTI FIN IIB-IIII RECEPTOR ON ADP, THROM	THE FAMILY (SINTEGRINS,	HINS; 1. TI, CELL ADHESION; V BY SIMILARITY. CELL ATTACHMENT 1; 242B63C4 CRC32;	Score 282; Pred. No. 7 12; Mismat	CCDQCRFMKKG' 	PRT;	CREATED) LAST SEQUENCE UI LAST ANNOTATION PLATELET AGGREGS PISCIVORUS (EA
аннаннянняннянняння		:	AST AST AST ATE IOFF	86	FIB	50	TELE MW	.78; .58; 1ve	AEGI SGF	ä	CREZ LASJ LASJ PLAJ PIS
478 478 833 833 677 677 677 677 677 677 677 677 677 6		ANDARE	18, 0 18, 1 24, I IN (PI BLOMP A; CHC		IBITS GLYCOF GLYCOF IB-II	ELONG	T. DISIN; PLAT ; PLAT 66 66 53 7517	y 52 ervat	QGAQCA :- :- EGEHCA	STANDARD;	~ 21
044646464646464646464646464646464646464		ST	1 (REL. 2 (REL. 2 (REL. N HALYS N HALYS METAZO.	OM; 1362676	SED ON ROTEIN	RITY: B	94; 183 800427; ULATION 47 51 71 AA;	Similarity 31; Conse	AATCKLR : 1 PVKCEPR		(RE (RE (RE A APP
2116 2112 2112 2112 2011 1002 1147 1177 1177 1177 1189 899 899 891 881 882 883		1 ISI_AGKHA 21858:	1-MAY-199 1-MAY-199 1-DEC-199 ISINTEGRI GKISTROTA; UKARYOTA;	EQUENCE. ISSUE-VEN EDLINE; 9 UANG TF	EXPRES AGGREG	I- SIMILA ANTAGO	SSE; F1/4 ROSITE; F LOOD COAG ISULFID ITE	y Match Local Si thes 31	13 NPCCD : 4 HPCCD	ISI_AGKPI	P10338; 01-AUG-1990 01-AUG-1992 01-DEC-1992 DISINTEGRIN
40000000000000000000000000000000000000		RESULT ID D	SCOOD A M J	R R R R R R R R R R R R R R R R R R R	388888	3888	S S S S S S S S S S S S S S S S S S S	Query Best 1 Match	oy op	50	Seedoo

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Query Match
Best Local Similarity
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P17496;
                                                                                                                                         62
                                                                                                               70 PF 71
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                          61
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                              Matches
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                                                                   CHAO B.H., JAKUBOWSKI J.A., SAVAGE B., PING CHOW E., MARZEC U.M.,
HARKER L.A., MARAGANORE J.M.;
PROC. NATL. ACAD. SCI. U.S.A. 86:8050-8054(1989).

1. FONCTION: INHIBITS FIBERNOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURPACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
AND COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEDISHER T.A., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEDISHER T.A., BUNTIOS S., LAZARUS R.A.,
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475 (1990).

- I. FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPEN ILB-ILIA COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN ILB-ILIA RECEPTOR ON THE PLATELET SUFFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-AMR-1992 (REL. 21, LAST ANNOTATION UPDATE)
01-SMAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
101SINTEGENI TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION
1NHIBITOR).
TRIMBERSCHUEUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).
EENKARYOTA: METAJOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA, SERPENTES.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                    13 NPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVC-RARGDDVNDYCNGISAGCPRNPF 70
                                                                                                                                                                                                                                                                                                                                                                                                   -:- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR: A31990; A31990.
HSSP: P17494; 1KST.
PROSITE: PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 65 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND COLLAGEN.
THE SEQUENCE SHOWN IS THAT OF TRICRAMIN BETA-2.
SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
C35982; C35982.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                          <del>.</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 278; DB 1; Length 71; Pred. No. 7.92e-47; 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                    CELL ATTACHMENT SITE.
                                                                                                                                                                                                                                                                                                 320595A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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(REL. 15, LAST SEQU
(REL. 21, LAST ANNO
                                                                                                                                                                                                                                                                                                                            52.0%;
larity 54.2%;
Conservative
                                                                                                                                                                                                                                                                                                  71 AA; 7522 MW;
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                                                                                                                                                                                                                                                                                                               1KST.
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                                                        90046735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P17495;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3
DISB_TRIGA
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                           SEQUENCE
                                                           MEDLINE;
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INT. J. PEPT. PROTEIN RES. 48:220-228(1996).
-1- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
-1- FUNCTION: INTERPRESED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LU W., COOK J.J., JAMESON B.A.,
                                                                          69
                                                                                          SPECIES-T.ALBOLABRIS;
MEDLINE: 94109384.
JASEJA M., SMITH K.J., LU X., WILLIAMS J.A., TRAYER H., TRAYER I.P.,
HYDE E.I.;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                 TRIMERESURUS GRAMINEÚS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE),
AND TRIMERESURUS ALBOLABRIS (WHITE-LIPPED PIT VIPER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM; E35982; E35982.
                                                                          10 SPANPCCDAATCKLLPGAQCGEGPCCDQCSFMKKGTICRRARGDDLDDYCNGRSAGCPRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.A.,
                                                                                                                                                                                                                                                                       01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DISINTEGRIN TRIGRAMIN GAMMA (ALBOLABRIN) (PLATELET AGGREGATION ACTIVATION INHIBITOR).
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-T.GRAMINEUS; TISSUE-VENOM;
MEDLINE; 90207217.
BENIS M.S., HENZEL W.J., PITII R.M., LIPARI M.T., NAPIER
DEISHER T.A., EUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
               Length 73;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S:
Score 275; DB 1; Len
Pred. No. 4.52e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P17494; IKST.
PROSITE: PS00427; DISIMTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULEID 6 15 PROBABLE.
DISULFID 8 16 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-T.ALBOLABRIS; TISSUE-VENOM;
MEDLIAMS, 90283463.
WILLIAMS, J., ROLINS, HOLT J., NIEWIAROWSKI
BIOCHIM. BIOPHYS. ACTA 1039:81-89(1990).
                                                                                                                                                                                                                             73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHAEFER W., SOSZKA T.,
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUR. J. BIOCHEM. 218:853-860(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30:5225-5229(1991).
                                                                                                                                                                                                                                                           01-AUG-1990 (REL. 15, CREATED)
                 51.4%;
                                                Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-T.ALBOLABRIS;
MEDLINE; 91242430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-T.ALBOLABRIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; S43021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97052455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND COLLAGEN.
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NIEWIAROWSKI S
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-:- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
                                                                                                                                  10 SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN 69
                                                                                                                                             Gaps
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1-FBE-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FBE-1995 (REL. 31, LAST ANDTATION UPDATE)
DISINTEGRIN ECHISTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92104150.
DALVIT C., WIDMER H., BOVERMANN G., BRECKENRIDGE R., METTERNICH
EUR. J. BIOCHEM. 202:315-321(1991).
                                                                                                                                                                                                                                                                                                                                                                                       FRIEDMAN P.A., POLOKOFF M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE, 92089067.
CHEN Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90207217.
DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
                                                                                                           ö
                                                                                                                                                                                                                                                                                     (CARINATIN)
ECHIE CARINATUS (SAW-SCALED VIPER)
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA: TETRAPODA; REPTILIA:
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P., WEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
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CALVETE J.J., WANG Y., MANN K., SCHAEFER W., NIEWIAROSKI
STEWART G.J.;
                                                                                  Score 267; DB 1; Length 73;
Pred. No. 4.63e-44;
13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92104151.
COOKE R.M., CARTER B.G., MARTIN D.M.A., MURRAY-RUST
EUR. J. BIOCHEM. 202:323-328(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92104152.
SAUDEK V., ATKINSON R.A., LEPAGE P., PELTON J.T.;
EUR. J. BIOCHEM. 202:329-338(1991).
                                               CELL ATTACHMENT SITE. DA64D759 CRC32;
                                                                                                                                                                                                              49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91308124.
SAUDEK V., ATKINSON R.A., PELTON J.T.;
BIOCHEMISTRY 30:7369-7372(1991).
                        PROBABLE
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
TISSUE-VENOM;
MEDLINE: 89066819.
GAN Z.R., GOULD R.J., JACOBS J.W., F'
J., BIOL. CHEM. 263:19827-19832(1988)
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOCHEMISTRY 30:11625-11636(1991)
35
59
38
66
53
7573 MW;
                                                                                 Ouery Match
Best Local Similarity 50.0%;
Matches 30; Conservative
                                                                                                                                                                                                              STANDARD;
                                                            73 AA;
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DISULFID
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SITE
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ACTIONNE, SOURCE VENDAGE TO TELEMBRICH SOURCE TISSUE VENDAGE TO TELEMBRICH SOURCE TISSUE VENDAGE TO THE TELEMBRICH SOURCE TO THE TEXPRESSED ON GLYCOPPOTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE GLYCOPPOTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND CC. INHIBITS AGGREGATION INDUCED BY ADP. THROWBIN, PLATELET ACTIVATING CC. INHIBITS AGGREGATION INDUCED BY ADP. THROWBIN, PLATELET ACTIVATING CC. INHIBITS AGGREGATION INDUCED BY ADP. THROWBIN, PLATELET ACTIVATING CC. INHIBITS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. ANTACONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. BROSTE: PSO0447; DISINTEGRINS; 1.

KW BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM. BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM. SEQUENCE 71 AA; 7637 MW; 910AFOZC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                          AGGREGATLAN
AND COLLAGEN
-:- THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
-:- THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
-:- SIMILARIYE; BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR, 332029; A35982.
PIR, 33198; S29198;
PIR, S29198; S29198;
PIR, S29198; S29198;
PIR, S29198; S29198;
PIR, S29198; S29198;
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM; 3D-STRUCTURE.
BLOOD—COAGULATION; PLATELET; CELL ADHESION; ALPHA-2.
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIAGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
COLJUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
COLJUL-1993 (REL. 26, LAST ANNOTATION ACTIVATION INHIBITOR).
CROTALUS VIRIDIS VIRIDIS (PRAIRIE FRATLESNAKE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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49.0%; Score 262; DB 1; Length 71;
Best Local Similarity 46.8%; Pred. No. 8.27e-43;
Matches 29; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 265; DB 1; Length 49;
Pred. No. 1.47e-43;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL ATTACHMENT SITE.
MISSING (IN ALPHA-2 FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QCESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKG 46
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PROBABLE.
PROBABLE.
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Local Similarity 71.7%;
nes 33; Conservative
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32
33
33
49
7
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P31987;
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DISULFID
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DISULFID
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SEQUENCE
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VARIANT
TURN
STRAND
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9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68

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TISSUE-VENOM
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                                                                                                                                                                                                                                 Query Match
Best Local
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Matches
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SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 208:1008-1005(1993).
-! FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZI L., ARRETEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: IMHIBITS FIBRANOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SUBFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
B13020: B43020.
HSSP, P14494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION: PLATELET; CELL ATTACHHENT SITE (POTENTIAL).
SITE
51
SITE
51
SA; 7781 MW; BFE2B942 CRC32;
                         9
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SSYHPCCDPVKCEPREGEHCISGPCCRNCYFLRAGTVCKRAVGDDVDDVCSGITPDCPRN
                                                                                                                                                                                                                                                                  01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN CEREBERIN (PLATELET AGREGATION ACTIVATION INHIBITOR).
CROTALUS VIKIDIS CEREBERUS (ARIZONA BLACK RATTLESNAKE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; TETRAPODA: REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (REL. 26, CREATED)
1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNORATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNORATION UPDATE)
DISINTEGRIN MOLOSSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS MOLOSSUS MOLOSSUS (NORTHERN BLACK-TAILED RATTLESNAKE).
EUKARNOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 261; DB 1;
Pred. No. 1.47e-42;
                                                                                                                                                                                                       72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AA
                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                   CREATED)
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Best Local Similarity 46.8%;
Matches 29; Conservative
                                                                                                                                                                                                       STANDARD;
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P31984;
01-JUL-1993 (REL. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93123215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-VENOM;
MEDLINE; 9312
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TISSUE-VENOM;
                                                                                                                                                                                                                                                   01-JUL-1993
                                                                                                                                                                               RESULT 7
ID DISI_CROVE
AC P31985;
DT 01-JUL-1993
DT 01-JUL-1993
DT 01-JUL-1993
DE DISINTEGRIN
OS CROTALUS VIR
                                                                                           l:
RY 62
                                                                 RF 70
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RY 62
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SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.,
J. BIOL. CHEM. 268:11085-1065(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED NG LYCOPROFIEN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROFIEN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
                       -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; H43019; H43019.
PASSP, P14444; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE (POTENTIAL).
SITE (POTENTIAL).
SEQUENCE 73 AA; 7880 MM; 7312E08D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE FAMILY OF GPITB-IIIA PROTEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. 143019.
PRSP: P17494; 1KST.
PROSITE: PS00427; DISINTEGRINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 NPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNRF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISI_CROBA STANDARD; PRT; 72 AA.
P31981;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
CROTALUS BASILICIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS BASILICUS (MEXICAN WEST-COAST RATTLESNAKE).
EUKARYOTA, METAZOA, CHORDATA, VENTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISI_LACMU STANDARD; PRT; 73 AA.
P31990;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION VPDATE)
101-SINTEGRIN LACHESIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
LACHESIS MUTA MUTA (BUSHMASTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                       ö
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BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 50 52 CELL ATTACHMENT SITE (POTENTIAL).
SEQUENCE 72 AA; 7704 MW; 4B255615 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                 Score 260; DB 1; Length 73;
Pred. No. 2.62e-42;
12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Pred. No. 8.21e-41;
15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                 1 48.6%;
Similarity 49.2%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity 45.2%;
es 28; Conservative
FACTOR AND COLLAGEN
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TISSUE-VENOM;
LT 12
DISI_BOTCO
P31988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISI_BOTJA
P31989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                       RY SEQUENCE.

RX MEDLINE; 9312315.

RX MEDLINE; 93123215.

RA SCARROROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,

RA SCARROROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,

RA J. BJOL. CHEM. 268:1058-1065(1993).

C. TUNCTION: INHIBITS FIRSHNOGEN INFRACTION WITH PLATELET RECEPTORS

C. EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE CLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND

C. CLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND

C. INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING

C. FACTOR AND COLLAGEN.

C. SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN

C. ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.

DR PRSSP: P17494; IKST.

DR RISSP: P17494; IKST.

DR RISSP: P17494; IKST.

DR ROSITE; PSO0427; DISINTEGRINS; 1.

FW BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

FY BLOOD COAGULATION; PLATELET; CELL ATPACHMENT SITE (POTENTIAL).

FT STTE.

TITE.

T. AA; 7765 MM; ORCSDEBO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RUCINSKI B., NIEWIAROWSKI S., HOLT J.C., SOSZKA T., KNUDSEN K.A.:
BIOCHIM. BIOPHYS. ACTA 1054:257-262(1990)
- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPIEN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISI_BOTAT STANDARD; PRT; 71 AA.
P18618;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINFECRIN BATROXOSTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BUTHROPS ATROX (BARBA AWARILLA) (FER-DE-LANCE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROFEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. PIR; S13168; S13168;
                                                                                                                                                                                                                                                                                                                                                   11 PANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                                                            Score 251; DB 1; Length 73;
Pred. No. 4.58e-40;
12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S13168; SILL.
HSSP; P17494; 1KST.
HRSP; P17494; 1KST.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 66
BY SIMILARITY.
66
BY SIMILARITY.
7602 MW; A73CFB7E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 250; DB 1;
Pred. No. 8.11e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.7%;
50.8%;
                                                                                                                                                                                                                                                                                               Match 46.9%;
Local Similarity 47.5%;
les 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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tes 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE: 9
RUCINSKI E
                                                                                                                                                                                                                                                                                                                                                                                                                71 Y 71
                                                                                                                                                                                                                                                                                                                                                                                                                                        62 Y 62
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Matches
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ARDLINE; 93123215.
RA MEDLINE; 93123215.
RA SCRRBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
RA DIAZIL L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
B. NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
CC -!- FUNCTION: INHIBITS FIBRINGOEN INTERACTION WITH PLATELET RECEPTORS
CC GLYCOPROTEIN ILB-IIIA COMPLEX. ACTS BY BINDING TO THE
CG CALYCOPROTEIN ILB-IIIA COMPLEX. ACTS BY BINDING TO THE
CC INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET ACTIVATING
CC FACTOR AND COLLAGEN.
CC FACTOR AND COLLAGEN TO THE FAMILY OF GPIIB-IIIA PROTEIN
CC -- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
CC -- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
DR RANDAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
DR RASP; P17464; 1KST.
DR PROSITE; PS00427; DISINTEGRINS; 1.
KW BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
FT DISULFID
FT SITE 73 AA; 7739 MW; 15EEAA7A CRC32;
CSC GELL ATTACHMENT SITE (POTENTIAL).
SEQUENCE 73 AA; 7739 MW; 15EEAA7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93123215.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., CHARO I.F.;
NANNIZZI L., ARESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1055(1993).
-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPIEN IIIB-IIIB-IIIB-IIIB-IIIS SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR AND COLLAGEN.
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIN: F44019; F43019
HSSP, P17494; 1KST.
PROSITE; PSO0427; DISINTEGRINS; 1.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISIULED 47 66
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL).
SITE 72 AA; 7709 MW; 0D73D088 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANDTATION UPDATE)
DISINTEGRIN JARARACIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEERIN COTIARIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
BOTHROPS COTIARA (COTIARA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOTHROPS JARARACA (JARARACA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 250; DB 1; Length 72;
Pred. No. 8.11e-40;
10; Mismatches 19; Indels
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72 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEPIDOSAURIA; SERPENTES
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ses 30; Conser
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HUANG T.-F., HOLT J.C., LUKASIEWICZ H., NIEWIAROWSKI S.;

J. BIOL. CHEM. 262:16157-16163(1987).

C. '- FUNCTION: THIS PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT

ACTS IN HEMORRHAGE (BY SIMILARITY).

C. '- FUNCTION: TRICRAMIN INHIBITS FIBRINOGEN INTERACTION WITH PLATELET

BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET

SURFACE AND INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN,

C. '- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR

PROTEOLYTIC ACTIVITY.

C. '- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC

METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.

C. '- SIMILARITY: HIGH, IN THE C-TERMINAL REGION, TO OTHER DISINTEGRINS.
                               ö
                                                                                                                                                                      01-APR'1990 (REL. 14, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
19-UTATIVE VENOM METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) (CONTAINS:
DISINTEGRIN TRIGRAMIN ALPHA (PLATELET AGGREGATION ACTIVATION
                                                                                                                                                                                                                                                      inaldiuki).
Trimeresurus gramineus (indian green tree Viper) (green habu snake).
Eukariota, metazoa; Chordata; vertebrata; tetrapoda; reptilia;
Lepidosauria; serpentes.
                                Gaps
                                                                       13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAPIER M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSO142: ZINC_PROTEASE; 1.
PSO1427; DISINTEGRINS; 1.
SE: METALLOPROTEASE; ZINC; BLOOD COAGULATION; PLATELET;
HESION; VENOM; ZYMOGEN; SIGNAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE ZINC METALLOPROTEINASE. TRIGRAMIN.
Score 250; DB 1; Length 73;
Pred. No. 8.11e-40;
10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC).(PROBABLE).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC (CATALYTIC) (PROBABLE)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DENNIS M.S., HERZEL W.J., PITTI R.M., LIPARI M.T., DEISHER T.A., BUNTING S., LAZARUS R.A., PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                     KIRBY E.P., NIEWIAROWSKI
                                                                                                                                                 Ą
                                                                                                                                                 480
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
MEDLINE 90332429.
NEEPER M.P., JACOBSON M.A.;
NUCLEIC ACIDS RES. 18:4255-4255(1990)
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 89229063.
HUANG T.-F., HOLT J.C., KIRBY
BIOCHEMISTRY 28:661-666(1989)
Ouery Match
Best Local Similarity 50.8%;
Matches 30; Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, XS1530; G64408;
PIR: A29784; A29784.
PIR, A30065; A30065.
HSSP, P34179; 11AG.
PROSITE: PS00141; ZINC. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL ADHESION; VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 408-479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 408-419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 408-479.
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408
333
334
337
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-VENOM
                                                                                                                                           DISA_TRIGA
P15503;
                                                                                                                                                                                                                                                INHIBITOR))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASE;
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ACT_SITE
METAL
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DISULFID
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NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
                                                                                                                                                                                           417 SPANPCCDAATCKLIPGAQCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCNGRSAGCPRN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FACTOR AND COLLAGEN.
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR: B43019; B43019.
PIR: D43019; D43019.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGTVCRPARGDWNDDTCTGQSADCPRN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DISINTEGRIN CROTATROXIN/DURISSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                             CROTALUS ATROX (WESTERN DIAMONDBACK RATTLESNAKE), AND CROTALUS
DURISSUS DURISSUS (CENTRAL AMERICAN RATTLESNAKE).
EURARYOTA; METAZOA: CHORDATA: VERTEBRATA; TETRAPODA; REPIILIA;
                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 249; DB 1; Length 480
Pred. No. 1.44e-39;
12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 233; DB 1; Length 72;
pred. No. 1.29e-35;
11; Mismatches 20; Indels
BY SIMILARITY.
CELL ATTACHMENT SITE.
POTENTIAL.
                                                                                                                 D59DA91F CRC32;
                                                                                                                                                                                                                                                                                                                         72 AA.
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                  53494 MW;
                                                                                                                                          Query Match 46.5%;
Best Local Similarity 46.8%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEPIDOSAURIA; SERPENTES
  353
4442
4445
4445
4466
279
                                                                                                                  480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 29: Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93123215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-VENOM;
                                                                                                                                                                                                                                             477 PF 478
                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                       DISI_CROAT
                                                  DISULFID
DISULFID
DISULFID
               DISULFID
  DISULFID
                                      DISULFID
                                                                                                    CARBOHYD
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Search completed: Fri Sep 25 13:10:30 1998 Job time : 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 5.47 Seconds 198.250 Million cell updates/sec Fri Sep 25 13:11:55 1998; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output

not generated

>PCT-US98-16719-2

(1-67) from PCTUS9816719A.pep 535 Description: Perfect Score:

1 NSVHPCCDPVKCEPREGEHC........DXCSGITPDCPRNRXKGKED 67 Seguence:

Scoring table:

Searched:

PAM 150 Gap 11

131922 segs, 16180660 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq32
i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Mean 25.292; Variance 97.479; scale 0.259 Statistics:

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Ouery	Ouery Match Length DB	DB	a	Description	Pred. No.
п	294	55.0	73	23	W14083	Platelet aggregation	9.70e-21
7	293	54.8	73	~	R06494	Platelet aggregation	1.23e-20
m	282	52.7	97	Ŋ	R28708	Bifunctional inhibito	1.74e-19
4	282	52.7	86	ഹ	R25154	Bifunctional inhibito	1.74e-19
S	282	52.7	480	æ	R42867	Platelet aggregation	1.74e-19
ø	278	52.0	96	ហ	R28707	Bifunctional inhibito	4.53e-19
7	278	52.0	97	ហ	R28706	Bifunctional inhibito	4.53e-19
80	278	52.0	66	S	R25153	Bifunctional inhibito	4.53e-19
σ	278	52.0	106	'n	R25152	Bifunctional inhibito	4.53e-19
10	277	51.8	71	10	R53942	Disintegrin peptide #	5.76e-19
11	276	51.6	97	Ŋ	R28705	Bifunctional inhibito	7.32e-19
12	276	51.6	86	ა	R25150	Bifunctional inhibito	7.32e-19
13	275	51.4	72	ო	R10109	Trigramin-beta 1	9.30e-19
14	275	51.4		m	R10110	Trigramin-beta 2.	9.30e-19
15	274	51.2	96	'n	R25382	Bifunctional inhibito	1.18e-18
16	274	51.2		'n	R25151	Bifunctional inhibito	1.18e-18
17	272	50.8	96	Ŋ	R28703	Bifunctional inhibito	1.91e-18
18	272	50.8	97	ហ	R28704	Bifunctional inhibito	1.916-18

1.91e-18 1.91e-18	근근	.30e-1	.30e-1	ო.	1.02e-17	७.	2.64e-17	٠.	4	.64	4	m	3.35e-17	φ.	٦.	3.62e-16	.62e-1	.59e-1		.36e-1	36	e-1	88	3.88e-15
	Bifunctional inhibito Albolabrin peptide ta	딒	9	Albolabrin.	Echistatin-alpha 2.	Platelet adhesion blo	44	Wild type disintegrin	റ	rin peptid	Platelet adhesion blo	Sequence of viper ven	귝	Sequence of viper ven	in with As		Disintegrin peptide #	~	per	ad)		of viper	of viper	4-10
R25149 R25148	R25147 W45500	R53946	R10106	R06395	R10113	R24287	R06388	W02647	P91088	R53938	R24288	P91098	R12986	P91099	R34291	R06396	R53940	P91320	P91094	R24289	P91095	P91096	2	R46949
ហស	28 28	10	m	a	m	7	-	18	4	10	N	4	m	4	ဖ	N	9	Н	4	~	4	4	4	ω
106	736	73	73	73	47		49	49	49	49	49	49	49	49	49	71	71	72	49	49	49	49	49	28
50.8 50.8		6	σ,	49.9	œ.	œ	48.8	٠	œ.		œ.	œ.	48.6		7.	ė.		ė.	ů.	ė		45.2	٠	44.9
272	267	267	267	267	265	261	261	261	261	261	261	260	260	256	255	250	250	249	247	246	246	242	240	240
13 20 3	22	23	24	22	26	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	42

ALIGNMENTS

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TAY-1007.

10.54N-1997.

24-AGC-1995; RR-019685.

PA (MCGA-) MOGAM BIOTECHNOLOGY RES INST.

(MCGA-) MOGAM BIOTECHNOLOGY RES INST.

PA (MAKI-) ZH MAKIIMA SEIMEI KOGAKU KENKYUSHO.

PA (MAKI-) ZH MAKIIMA SEIMEI KOGAKU KANAN SEIMEN SAIMEN SAIMEN AND SAIMEN SA
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                                                          W14083;
27-0CT-1997 (first entry)
Platelet aggregation inhibitor, Salmosin.
Salmosin; inhibit; blood; platelet aggregation; venom; Korean;
salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.
Agkistrodon halys brevicaudus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 294; DB 23; Length 73;
Pred. No. 9.70e-21;
13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 2
R06494 standard; protein; 73 AA.
R06494.
04-JAN-1991 (first entry)
Platelet aggregation inhibitor.
Snake venom; thromboxan A2; thrombosis; anti-coagulant.
                                  standard; peptide; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.0%;
Best Local Similarity 52.5%;
Matches 31; Conservative
LT 1
W14083 :
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ID RC
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97 AA;
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                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprise glyco-protein lib or line and thrombin inhibitory
moieties, for treating thrombotic diseases, atherosclerosis,
cancer and neuroiedenerative conditions

Claim 7: Page 25: 103pp: English
Clai
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Bifunctional inhibitor of platelet activation and thrombin #14.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 npccdaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpf 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and new recombinant DNA encoding it.

Claim 3: Fig 9: 73pp: English.

The sequence is deduced from the coding strand of a synthetic
gene for a polypeptide inhibitor of platelet activation. The
polypeptide is analogous to that obtd. from the venom of
Agkistrodon p. piscivorus (North American Water Moccasin). The
gene can be used to produce recombinant inhibitor or fusion
proteins with eg. hirudin derivs. These can be used to decrease/
inhibit platelet aggregation and release in vivo or in vitro.
Usual dose is 0.01-100 mg/kg body wt. The recombinant protein can
also be used to coat the surfaces of invasive medical devices.
                                                                                                                                                                                                                                      Pure platelet activation inhibiting polypeptide from snake venom - used for preventing agglutination and release in vivo or vitro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in can also block stenosis and spasm at the site of thrombosis (by inhibiting the release of thromboxan A2 ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 92-214630/28.
Bi:functional inhibitors of thrombin and platelet activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chao BH, Maraganore JM, Strauch KL, Thompson JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 293; DB 2;
Pred. No. 1.23e-20;
                                                                                                                                                                      Maraganore JM, Jakubowski JA, Chao BH; WPI; 90-260891/34.
N-PSDB; Q05730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 3
R28708 standard; Protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.8%;
Similarity 54.2%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
                                                     26-JAN-1990; U00465.
27-JAN-1989; US-303590.
27-JAN-1989; US-303585.
01-NOV-1989; US-430313.
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Best Local Similarity
                                                                                                                                    (BIOG-) BIOGEN INC. (UYBO-) BOSTON UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC
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                                     09-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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The first comprise glyco:protein IIB or IIIa and thrombin inhibitory

comprise glyco:protein IIB or IIIa and thrombin inhibitory

moleties, for treating thrombotic diseases, atherosclerosis,

cancer and neuro:degenerative conditions

Claim 7: Page 25: 103pp; English.

The sequence represents the bifunctional inhibitor of platelet

activation and thrombin, and is referred to as IIe-Met-Cappilog(leu41)

The inhibitor also contains a thrombin inhibiting component. The
inhibitor is used to inhibit thrombin and platelet-mediated processes
in patients or in extracorporeal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombocytopaenia. The usual dose is
lug-5mg/kg/day opt. combined with a thrombolytic agent such as
tissue plasminogen activator. The inhibitor may be used to treat
or prevent myocardial infarction, or thrombosis; increase reocclusion
time; decreasing reperfusion time; and inhibiting metastatic cell
correct.
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                                                                                                                                                                                                                                           14 npcddaatcklrpgagcaeglccdgckflkegtvcrrargddvndycngisagcprnpfh 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-1993 (first entry)

Bifunctional inhibitor of platelet activation and thrombin #13.

Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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THE STATE OF THE STATE 
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                                                                                                                                  10; Mismatches 18; Indels
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05-DEC-1991; U09108.
07-DEC-1990; US-623611.
(BIOJ ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
Score 282; DB 5;
Pred. No. 1.74e-19;
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R42867 standard; Protein; 480 AA.
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Best Local Similarity 54.1%;
Matches 33; Conservative
                                                              Best Local Similarity 54.1%;
Matches 33; Conservative
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Seguence

Query Match Best Local 3

4atches

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R25153 standard; Protein; 99 AA.
R28706 standard; Protein; 97 AA.
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Best Local Similarity 52.5%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                  W09210575-A.
25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
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07-DEC-1990; US-6236
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                                                                                                                                                                                                                                                                                                          Synthetic
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moleties, for treating thrombotic diseases, atherosclerosis,
cancer and neuro:degenerative conditions
claim 7; Page 24; 103pp; English conditions
claim 7; Page 24; 103pp; English
component of platelet
activation and thrombin, and is referred to as Met-C-apping
The inhibitor also contains a thrombin and platelet-mediated processes
in patients or in extracorporeal blood. It inhibits clot formation
in patients or in extracorporeal blood. It inhibits clot formation
cand growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombocytopaenia. The usual dose is
lug-5mg/Kg/day opt. combined with a thrombolytic agent such as
tissue plasminogen activator. The inhibitor may be used to treat
or prevent myocardial infarction, or thrombols; increase reocclusion
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Bifunctional inhibitor of platelet activation and thrombin #11.
bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing resculusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 npccdaatcklrggaqcaeglccdqcrfmkkgtvcrlargddmddycngisagcprnpf 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpfh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                  The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    time; decreasing reperfusion time; and inhibiting metastatic cell
growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
                                                                                                                                   WPI; 93-348481/44.

N-PSDB; Q50394.

Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.

Example: Page 33-35; 50pp; Japanese.

The sequence is that of a polypeptide which inhibits platelet

The sequence is that of a nolypeptide which inhibits platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 282; DB 8; Length 480;
Pred. No. 1.74e-19;
12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches 18; Indels
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Chao BH, Maraganore JM, Strauch KL, Thompson JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.53e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 6
R28707 standard; Protein; 96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%;
larity 52.5%;
Conservative
                       26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE ) TAKEDA CHEM IND LTD.
WPI: 93-348481/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 52.5%;
les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1991; U09108.
07-DEC-1990; US-623611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 AA;
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25-JUN-1992 Synthetic.

v

64

RESULT

Sequence

Query Match

Best Loc Matches

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Tomprise glyco:protein IIB or IIIa and thrombin inhibitory

moleties, for treating thrombotic diseases, atherosclerosis,
cancer and neuroidegenerative conditions

To claim 7: Page 24: 103pp; English.

Claim 7: Page 24: 103pp; English.

This sequence represents the blfunctional inhibitor of platelet
activation and thrombin, and is referred to as C-appilog

The inhibitor also contains a thrombin inhibiting component. The
inhibitor is used to inhibit thrombin and platelet-mediated processes
in patients or in extracorporeal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombocytopaenia. The usual dose is
tissue plasminogen activator. The inhibitor may be used to treat
or prevent myocardial infarction, or thrombosis, increase recclusion 04-JAN'1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #12.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
W09210575-A. 04-JAN 1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #10.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth. cancer and neuro:degenerative conditions
Claim 7; Page 24; 103pp; English.
This sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as Ala-Asn-Ser-C-appilog
The inhibitor also contains a thrombin inhibiting component. The 14 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpfh 73 Gaps time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80. ö Chao BH, Maragance JM, Strauch KL, Thompson JS;
WPI: 92-234630/28.
BH:functional inhibitors of thrombin and platelet activation comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis, Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28. Bi:functional inhibitors of thrombin and platelet activation Score 278; DB 5; Length 97; Pred. No. 4.53e-19; 11; Mismatches 18; Indels

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Disintegrin peptide #10.
Disintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen; integrin binding sites; GP IIb/IIIs; human; platelets; radiolabel; treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli; tumours; abscesses; thrombus component.

Agkistrodon piscivorous

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.r 10 R53942 standard; peptide; 71 R53942;

(first entry)

21-DEC-1994

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inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bifunctional inhibitors of thrombin and platelet activation comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions

Claim 7: Page 24: 103pp; English.
This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as Cly-Ser-IIe-Glu-Gly-Arg-Pro-Glu-Phe-Met-C-appling
The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deposition, but do not cause thrombocytopaenia. The usual dose is 11g-7am/fxg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bifunctional inhibitor of platelet activation and thrombin #9. bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
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                                                                                                                                                                                                                                                                                                           decreasing reperfusion time; and inhibiting metastatic cell
1. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
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Pred. No. 4.53e-19;
11; Mismatches 18; Indels
                                                                                                                                                                                                           Score 278; DB 5; Length 99;
Pred. No. 4.53e-19;
11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R25152 standard; Protein; 106 AA.
                                                                                                                                                                                                           52.0%; silarity 52.5%; Conservative
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52.5%;
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07-DEC-1990; US-623611.
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Best Local Similarity (
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) BIOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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cancer and neuro:degenerative conditions
Claim 5: Page 24: 103pp; English.
This sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as N-appilog(Leu65).
The inhibitor also contains a thrombin inhibiting component. The
inhibitor is used to inhibit thrombin and platelet-mediated processes
in patients or in extracorporeal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombooytopaenia. The usual dose is
                                                                                                                                                                                                                                                                                                                                                                          Claim 24; Page 46; 62pp; English.

The sequences given in R53933-46 are disintegrin peptides.
Disintegrins are low molecular weight proteins from the Viperidae family of snakes which bind integrin proteins similar to the endogenous messenger and structurally interactive molecules.
Disintegrins are competitive inhibitors of biomolecules, such as fibrinogen, for integrin binding sites such as GP IIb/IIIa on human platelets. Disintegrins contain the tripeptide sequence Arg Gly-Asp. Radiolabelled disintegrin peptides can be used for the treatment and diagnosis of venous and arterial thrombi, pulmonary emboli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04.7AN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #7.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accreding fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 npccdaatcklrpgaqcaqglccdqckfmkegtvc-rargddvndycngisagcprnpf 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis,
                                                                                                                                                                                                                                                                                                                     disintegrin(s) - for treatment and diagnosis of venous and arterial thrombi, pulmonary emboli and tumours or abscesses having a thrombus component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                                                                                                                                                                                     Radio-labelled polypeptide(s) derived from Viperidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           component
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Chao BH, Maraganore JM, Strauch KL, Thompson JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 277; DB 10;
Pred. No. 5.76e-19;
10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumours or abscesses that have a thrombus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 11
R28705 standard; Protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 51.8%;
Similarity 54.2%;
32; Conservative
                                                                                                                                                                                             05-0CT-1992; US-965674. (UTEM ) UNIV TEMPLE. Knight LC, Maurer AH:
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05-DEC-1991; U09108.
07-DEC-1990; US-623611.
                                                                                                                                                                                                                                                              Knight LC, Maurer AH; WPI; 94-151248/18.
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"This functional inhibitors of thrombin and thrombin inhibitory

"This profit the process of thrombotic diseases, atherosclerosis,

"This sequence represents the bifunctional inhibitor of platelet

"The inhibitor also contains a thrombin inhibiting component. The

"Inhibitor is used to inhibit thrombin and platelet-mediated processes

inhibitor is used to inhibit thrombin and platelet-mediated processes

in patients or in extracorporeal blood. It inhibits clot formation

and growth caused by platelets and clot accretion caused by fibrin

and growth caused by platelets and clot accretion caused by fibrin

and growth caused by platelets and clot accretion caused by fibrin

and growth caused and clot accretion acused by fibrin

and stown prografial infarction, or thrombolytic agent such as

tissue plasminogen activator. The inhibitor may be used to treat
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lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
                                                                                                                                                                                                                                                                                            04.JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #6.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                           0; Gaps
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                time; decreasing reperfusion time; and inhibiting metastatic cell
growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition; GP IIA; GP IIIA; hypercoagulation. Trimesurius gramineus.
                                                                                                            Length 97;
                                                                                                         Score 276; DB 5; Length 97;
Pred. No. 7.32e-19;
10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 276; DB 5; Length 98;
Pred. No. 7.32e-19;
10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOJ ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
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R25150 standard; Protein; 98 AA.
R25150;
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llarity 54.2%;
Conservative
                                                                                                         51.6%;
Similarity 54.2%;
32; Conservative
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13-MAR-1991 (first entry)
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05-DEC-1991; U09108.
07-DEC-1990; US-623611.
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07-JUN-1990; U03216.
07-JUN-1989; US-362718.
                                                                                                                       Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                              97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #15.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing recocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                 Disclosure; Fig 11; 91pp; English.

The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.

See also R10106-R10113
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The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.
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(GETH ) GENENTECH INC.
Lazarus RA, Dennis MS;
WPI: 91-007159/01.
Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
Lazarus RA, Dennis MS;
WPI; 91-007159/01.
Platelet aggregation inhibiting amino acid sequences - are
derived from snake venom and inhibit fibrinogen binding to
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Pred. No. 9.30e-19;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                  Score 275; DB 3; Length 72;
Pred. No. 9.30e-19;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               т 14
R10110 standard; Protein; 73 AA.
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Best Local Similarity 48.4%;
Matches 30; Conservative
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Best Local Similarity 48.4%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1990.
07-JUN-1990; U03216.
07-JUN-1989; US-362718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trimesurius gramineus. WO9015072-A.
                                                                                                                                                                                                                                                   72 AA;
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                                                                                                              IIA-GP IIIA.
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04-JAN-1993
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PF 05-DEC-1991; U09108.

N-DEC-1990; US-623611.

PA (BLOJ) BIOGEN INC.

Chao BH, Maraganore JM, Strauch KL, Thompson JS;

WPI: 92-234630/28.

Brifunctional inhibitors of thrombin and platelet activation -

DR anithmetical inhibitors of thrombin inhibitory

Tomprise glyco:protein IIB or IIIa and thrombin inhibitory

Tomperson and neuro:degenerative conditions

PT cancer and neuro:degenerative conditions

Claim 9a; Page 76; 103pp; English.

Claim 9a; Page 76; 103pp; Cancer and clot accretion caused by fibrin deposition, but do not cause thrombosylopaenia. The usual dose is tissue plasminogen activator. The inhibitor may be used to treat correspondent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R5142-54 R5382,3, Q25314,5 Q25884-90, Q31179,80.
Synthetic.
WO9210575-A.
25-JUN-1992.
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ö 0; Gaps Score 274; DB 5; Length 96; Pred. No. 1.18e-18; 10; Mismatches 19; Indels Query Match
Best Local Similarity 52.5%;
Matches 32; Conservative g ò

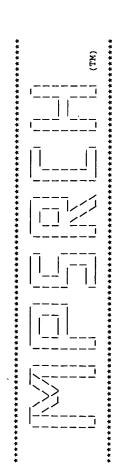
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Search completed: Fr1 Sep 25 13:12:14 1998 Job time : 19 secs.

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srch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Sep 25 13:10:50 1998; MasPar time 7.05 Seconds 400.042 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-2 (1-67) from PCTUS9816719A.pep 535 Description: Perfect Score:

67

1 NSVHPCCDPVKCEPREGEHC......DYCSGITPDCPRNRYKGKED

Scoring table:

Sequence:

140555 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb16 Database:

1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mho 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_vtrus 12:sp_vertebrate 13:sp_unclassified

Mean 33.501; Variance 53.233; scale 0.629 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query	Query Match Length DB	g	£	Description	Dang.
			6	} :			Trees No.
г	413	77.2	478	12	098995	LEBETASE LE3 PRECURSOR	2.03e-78
7	282	52.7	480	12	090220	PREPRO-HALYSTATIN PREC	6.31e-46
Э	281	52.5	117	12	090221	PREPRO-HALYSTATIN 2 (F	1.10e-45
4	245	45.8	115	12	090222	PREPRO-HALYSTATIN 3 (F	4.94e-37
S	229	42.8	. 481	12	991505	PRO-TRIMUCIN PRECURSOR	3.04e-33
9	224	41.9	106	12	042593	MEMBRANE ANCHORED META	4.55e-32
7	220	41.1	789	10	P70505	FERTILIN ALPHA.	3.94e-31
æ	219	40.9	620	12	042138	METALLOPROTEINASE-DISI	6.75e-31
6	215	40.2	487	12	092119	ATROLYSIN E PRECURSOR	5.79e-30
10	215	40.2	735	4	028478	FERTILIN BETA.	5.79e-30
11	215	40.2	735	4	028472	FERTILIN BETA.	5.79e-30
12	211	39.4	777	10	060472	CELLULAR DISINTEGRIN-R	4.94e-29
13	209	39.1	616	12	090495	ECARIN PRECURSOR.	1.44e-28
14	209	39.1	814	~	013444	METARGIDIN PRECURSOR.	1.44e-28
15	209	39.1	814	~	013493	MDC15.	1.44e-28
16	208	38.9	792	7	019061	FERTILIN ALPHA-II (FRA	2.45e-28
17	205	38.3	735	~	P78326	FERTILIN BETA (FRAGMEN	1.21e-27
18	202	38.3	735	~	596660	FERTILIN BETA.	1.21e-27
19	204	38.1		2	060813	FERTILIN ALPHA (PH-30	2.07e-27
20	204	38.1	617	12	090499	METALLOPROTEASE.	2.07e-27

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098955
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
LEBETASE LE3 PRECURSON.
MACROVIPERA LEBETINA (LEVANTINE VIPER).
EUPIDOSAURIA: SOURMATAL EURKARYOTES; METAZOA; CHORDATA; UEPIDOSAURIA: SOURMATAL SCLEROGIOSSA; SERPENTES; COLUBROIDEA; VIPERINAE; MACROVIPERA.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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P SEQUENCE FROM N.A.
ACTISSUE-VEROM GLAND;
RL SIGGRE. JAASPOLLU A., TU A.T., SIIGGR J.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 224:229-236(1996).
DR EMBL; X97894; E246059;
DR PROSITE; PS00427; DISINTEGRINS; I.
SIGNAL: BLOOD COAGULATION; PLATELET: CELL ADHESION; VENOM. SIGNAL: 1 18 POTENTIAL.
FT SIGNAL
194 478 POTENTIAL.
FT SIGNAL 194 478 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                     / Match 77.2%; Score 413; DB 12;
Local Similarity 79.4%; Pred. No. 2.03e-78;
hes 50; Conservative 7; Mismatches 6;
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Matches
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EMBL; D28871; G559299; -.
PROSITE; PS00427; DISINTEGRINS; 1.
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                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LIVER;
FUJISMA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
TAKEDA KENKYUSHO HO 53:39-56(1994).
EMBL; D28871; G559298; -
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
                               SEQUENCE FROM N.A.

TISSUE=VENOM GLAND;

FUJISHWA Y., KORDA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;

TAKEDA KENKYUSHO HO 53:39-56(1994).

EMBL: D28870; G469190; --

PROSITE; PS00427; DISINTEGRINS; 1.

SIGNAL; BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUJISAWA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
TAKEDA KENKYUSHO HO 53:39-56(1994).
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  EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILLA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
                                                                                                                                                                         Length 480;
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EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTII
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE
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01-NOY-1996 (TREWBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREWBLREL. 05, LAST ANNOTATION UPDATE)
PREPRO-HALYSTATIN 3 (FRAGMENT).
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LAST ANNOTATION UPDATE)
                                                                                                                                                                     Score 282; DB 12; L
Pred. No. 6.31e-46;
12; Mismatches 16;
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LAST SEQUENCE UPDATE)
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Pred. No. 1.10e-45;
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68983596 CRC32;
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Best Local Similarity 49.2%; Pred. No. 1
Matches 30; Conservative 13; Mismat
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01-NOV-1996 (TREMBLREL. 01, LAST
01-JAN-1998 (TREMBLREL. 05, LAST
PREPRO-HALVSTATIN 2 (FRAGMENT).
AGKISTRODON HALYS.
                                                                                                                                                53619 MW;
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                     Ouery Match 52.7%;
Best Local Similarity 52.5%;
Matches 31; Conservative
                                                                                                                           391
480
                                                                                                                                    392 4
480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 F 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 Y 62
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                          T 3
Q90221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 4
                                                                                                                SIGNAL
                                                                                                                            CHAIN
                                                                                                                                        CHAIN
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MEMBRANE ANCHORED METALLOPROTEASE, DISINTEGRIN, CYSTEINE-RICH PROTEIN
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                                                                                                                                                                                                                                                        XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUB-SNAKE VENOM GLAND;
EMBL; X77089; G467704;
PROSITE; PSO0427; DISINTEGRINS; 1.
SIGNAL; METALLOPROTEASE; BLOOD COAGULATION; PLATELET; CELL ADHESION;
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 HPCCDPVKCEPREGEHCISGPCCRNCYFLRAGIVCKRAVGDDVDDYCSGIIPDCPRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-TRIMUCIN PRECURSOR.
TRIMERESURUS MUCROSQUAMATUS (TAIWAN HABU).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 NPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRCTGQSADCPRN
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                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.9%; Score 224; DB 12; Length 706;
40.0%; Pred. No. 4.55e-32;
ative 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 229; DB 12; Length 48
Pred. No. 3.04e-33;
10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-TESTIS;
SHILLING F.M., KRAETZSCHWAR J, GAYKO U., CAI H., WESKAMP
LEIBOW L., MYLES D.G., NUCCITELLI R., BLOBEL C.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 178185, G2231331;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINANA, (191505) PRELIMINANA, (191505) (191505) (1916) (TREMELREL. 01, LAST SEQUENCE UPDATE) (1916) (TREMELREL. 05, LAST ANNOTATION UPDATE) (1916) (1916) (1916) (1917) (1917) (1917) (1917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-7AN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM
                                                                                                                                        Score 245; DB 12; L
Pred. No. 4.94e-37;
11; Mismatches 18;

        SIGNAL
        1
        18
        POTENTIAL.

        CHAIN
        19
        481
        PRO-TRIMUCIN.

        SEQUENCE
        481
        AA, 54079
        MW, 23A332F0
        CRC32;

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SEQUENCE 706 AA; 79275 MW; 8992584A CRC32;
                                                           NON_TER 1 1 1 SEQUENCE 115 AA; 12389 MW; C10C6FAF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                           Query Match
Best Local Similarity 50.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.8%;
Best Local Similarity 49.1%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 40.0%;
Matches 24; Conservative
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SEQUENCE
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092119;
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Q28478
Q28478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                      SO THE ENERGY OF THE PROPERTY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCCDPVKCEPREGEHCISGPCCRNCYFLRAGTVCKRAVGD-DVDDYCSGITPDCPRNRYK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AC 042138

AC 042138

AC 042138

AC 042138

CO 1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DE METALLOPROTEINASE-DISINFEGRIN-LIKE PROTEIN UPDATE)

DE METALLOPROTEINASE-DISINFEGRIN-LIKE PROTEIN (EC 3.4.24.1).

OS ACKISTRODON CONTORTRIX LATICINCTUS.

C LEPIDOSAURIA; SERPENTES.

(1)

RP SEQUENCE FROM N.A.

RX MEDLINE; 95314311.

RA DE ARAUJO H.S., OWNBY C.L.;

RA DE RABUJO H.S., OWNBY C.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ADHESION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 219; DB 12; Length 620;
Pred. No. 6.75e-31;
12; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220; DB 10; Length 78
Pred. No. 3.94e-31;
12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y08616; E274094; -..
SPERM; TRANSMEMBRANE.
                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           789 AA; 86140 MW; 242203E2 CRC32;
                                                                                                                                     Ŗ.
                                                                                                                                 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY; TISSUE-TESTIS;
                                                                                                                                     PRT;
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                                                                                                                                 PRELIMINARY;
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Local Similarity 43.3%;
les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 44.3%;
Matches 27; Conservative
                                                                                                                                                                                             01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                      FERTILIN ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 M 523
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                                                                                              RESULT 7
ID P70505
AC P70505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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TISSUE-VENON GLAND:

(X) FED COURSE FROM N.A.

(X) MUDGLINE; 96067555.

(X) HUANG K.F., HUNG C.C., PAN F.M., CHOW L.P., TSUGITA A., CHIOU S.H.;

(Y) HUANG K.F., HUNG C.C., PAN F.M., CHOW L.P., TSUGITA A., CHIOU S.H.;

(Y) HUANG K.F., HUNG C.C., PAN F.M., CHOW L.P., TSUGITA A., CHIOU S.H.;

(Y) HUANG K.F., HUNG C.C., PAN F.M., CHOW L.P., TSUGITA A., CHIOU S.H.;

(Y) HUANG K.F., HUNG C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(Y) HOOLEM C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(Y) HOOLEM C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(X) HALALING C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(X) HALALING C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(X) HALALING C.C., PAN F.M., CHOM L.P., TSUGITA A., CHIOU S.H.;

(X) HALALING C.C., PAN F.M., CHOM L.P., TSUGNAL C.C., CHOOLEM C.C., CHOM L.P., TSUGNAL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 CCDTATCRFKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGTSASCPENHF 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||||: | | | :| | | | | | 4 HPCCDPVKCEPREGEHCISGPCCRNCYFLRAGIVCKRAVGDDVDDYCSGITPDCPRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 NPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRSTGQSADCPRN
                                                           01-00V-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
ATROLYSIN E PRECURSOR (EC 3.4.24.44) (CROTALUS ATROX
METALLOENDOPEPTIDASE E) (HEMORRHAGIC TOXIN E) (FRAGMENT).
TRIMBERSURUS MUCKOSQUAMATUS (TAIWAN HABU).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 215; DB 12; Length 48
Pred. No. 5.79e-30;
10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 4; Length 735
Pred. No. 5.79e-30;
13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-TESTIS;

MEDLINE; 95260313.

PERRY A.C.F.

BIOCHEM. J. 307:843-850(1995).

EMBL; X77653; G794077; -...

EMBL; X77653: G794077; -...

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM. SEQUENCE 735 AA; 82358 MW; F31BBC91 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8477DBFF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             735 AA
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487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 PO
398 PO
54782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-JAN-1998 (TREMBLREL. 05,
FERTILIN BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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PRELIMINARY;
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Best Local Similarity 37.9%;
Matches 22; Conservative
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Conservative
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196 3
487 AA;
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Les 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q28472
Q28472;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                413 CCDIAICRFKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGISASCPENHF 470
                                                                                                                                                                                                                           CELLULAR DISINTEGRIN-RELATED PROTEIN. EXTRACELLULAR (POTENTIAL).
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
FERTILIN BETA.
MACAGA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                      Score 215; DB 4; Length 735;
Pred. No. 5.79e-30;
13; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                                   CAVIA PORCELLUS (GUINEA PIG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-TESTIS;
WDLSBERG T.G., STRAIGHT P.D., GERENA R.L., HUOVILA A.-P.,
WDLSBERG T.G., WILES D.G., WHITE J.M.;
DEV. BIOL. 169:378-383(1995).
-! SUBCLILULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-! SIMILARITY: CONTAINS I BGF-LIKE DOMAIN.
EMBL. U22060; G965006;
SIGNAL; GLYCOPROTEIN; EGF-LIKE DOMAIN; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                               01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
CELLULAR DISINTEGRIN-RELATED PROTEIN PRECURSOR (ADAM 5).
                                                                                  SEQUENCE FROM N.A.

RAMARAO C.S., MYLES D.G., WHITE J.M., PRIMAKOFF P.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, U33959; G998340; -.

PROSITE: PS00427; DISINTEGRINS; 1.

BLOOD COAGULATION: PLATELET; CELL ADHESION; VENOM.
SEQUENCE 735 AA; 82372 MW; 8E68BAC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
DISINTEGRIN-LIKE.
CYS-RICH.
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 211; DB 10; L
Pred. No. 4.94e-29;
14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4C0FE54 CRC32;
                                                                                                                                                                                                                                                                              777 AA.
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POTENTIAL.
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                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                     Query Match 40.2%;
Best Local Similarity 37.9%;
Matches 22; Conservative
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Best Local Similarity 41.7%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566
634
777 AA;
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TRANSMEM
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CARBOHYD
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CARBOHYD
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260472
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-PROMONGS GLAND;
MEDLINE: 95151760.
NISHIDA S., FUJITA T., KOHNO N., ATODA H., MORITA T., TAKEYA H.,
KIDO I., PAINE M.J., KAWABATA S., IWANAGA S.;
BIOCHEMISTRY 34:1771-1778(1995).
EMBL: D32212; G717091; -.
090495
090495
090495
090495
0104045
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
ECARIN PRECURSOR.
ECHIS CARINATUS (SAW-SCALED VIPER).
EUGHS CARINATUS (SAW-SCALED VIPER).
EUGHS CARINATUS (SAW-SCALED VIPER).
EUGHDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METARGIDIN PRECURSOR.
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 209; DB 12; Length 616
Pred. No. 1.44e-28;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 209; DB 2; Length 814
Pred. No. 1.44e-28;
18; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                18 POTENTIAL.
616 ECARIN.
69462 MW; DE2FC9AA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9767B2E0 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRAETZSCHMAR J.R., LUM L., BLOBEL C.P.;
J. BIOL. CHEM. 271:4593-4596(1996).
EMBL; U41767; G1235674; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
METARGIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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29 814 ME
814 AA; 87686 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.3%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.1%;
Best Local Similarity 41.7%;
Matches 25; Conservative
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                191 6
616 AA;
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01-NOV-1996
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Q13493
Q13493;
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39.1%; Score 209; DB 2; Length 814;
Best Local Similarity 40.3%; Pred. No. 1.44e-28;
Matches 25; Conservative 18; Mismatches 17; Indels 2; Gaps
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                             [1]
SEQUENCE FROM N.A.
TISSUE-UMBILICAL VEIN;
MEDLINE; 97192141.
HERREN B., RAINES E.W., ROSS R.;
FASEB J. 11:173-180(1997).
EMBL; U46005; G1335872; -.
SEQUENCE 814 AA; 87716 MW; AZABFEZF CRC32;
SOR R R X X R R SO S
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59 RN 60

Search completed: Fri Sep 25 13:11:05 1998 Job time : 15 secs.

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protein - protein database search, using Smith-Waterman algorithm srch_pp

Fri Sep 25 13:16:25 1998; MasPar time 4.06 Seconds 413:572 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-19 (1-67) from PCTUS9816719A.pep 506 1 NSVHPCCDPVKCEPREGEHC......DYCSGITPDCPRNRYKXKXD 67 Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 33.891; Variance 51.954; scale 0.652 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARİES

Pred. No.	5.08e-45	5.05e-44	8.97e-44	8.73e-42	1.51e-40	2.67e-40	4.72e-40	8.33e-40	8.33e-40	8.33e-40	1.47e-39	1.42e-38	1.42e-38	7.78e-38	5.92e-33	1.03e-32	1.03e-32	1.03e-32	3.15e-32	3.15e-32	3.15e-32	7.31e-29	3.80e-28
<u>a</u>	HALYSIN (P	APPLAGIN (TRIGRAMIN	TRIGRAMIN	VIRIDIN (P	CEREBERIN	MOLOSSIN (BATROXOSTA	COTIARIN (JARARACIN	ECHISTATIN	BASILICIN	OM METALLO	LACHESIN (CROTATROXI	FLAVOSTATI	ELEGANTIN	TERGEMININ	LUTOSIN (P	BARBOURIN	CERASTIN (METALLOPRO	KISTRIN (P
Description	DISINTEGRIN	PUTATIVE VENOM METALLO	DISINTEGRIN	HEMORRHAGIC	DISINTEGRIN																		
DI DI	DISI_AGKHA	DISI_AGKPI	DISB_TRIGA	DISG_TRIGA	DISI_CROW	DISI_CROVE	DISI_CROMM	DISI_BOTAT	DISI_BOTCO	DISI_BOTJA	DISI_ECHCA	DISI_CROBA	DISA_TRIGA	DISI_LACMU	DISI_CROAT	DISI_TRIFL	DISI_TRIEL	DISI_SISTE	DISI_CROVL	DISI_SISBA	DISI_CROCC	HRTE_CROAT	DISI_AGKRH
DB	-	-	Н	Н	Н	Н	н	-	-1	Н	-	Н	-	Н	-	Н	-	Н	Н	Н	-	П	7
% Query Match Length	71	71	73	73	71	72	73	7.1	72	73	49	72	480	73	72	99	73	73	73	73	73	478	99
& Query Match	53.6	52.8	52.6	51.0	50.0	49.8	49.6	49.4	49.4	49.4	49.2	48.4	48.4	47.8	43.9	43.7	43.7	43.7	43.3	43.3	43.3	40.5	39.9
Score	271	267	266	258	253	252	251	250	250	250	249	245	245	242	222	221	221	221	219	219	219	202	202
Result No.	1	7	m	4	'n	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.80e-28 3.02e-28 3.02e-28 3.02e-28 3.02e-28 3.02e-28 3.02e-28 3.02e-28 5.02e-28 5.02e-28 5.02e-28 6.03e-28 7.04e-28 7.04e-23 7.05e-60 7.06e-28 7.06e-	4.18e-02
	ALPHA-AMYLASE SALIVARY
DISC_TRIFL DISR_AGKRH DISI_BITAR DISI_BITAR DISI_ERIMA DISJ_RET_TRIFL DISJ_BOTJA MS2_MOUSE MS2_MOUSE MS2_HORA MT2_CALSI MT2_CALSI MT2_CALSI MT2_SCYSE TRBM_HUMAN MT2_SCYSE VV_PI4HB TRBM_HUMAN MT2_STREE VV_PI4HB TREM_HUMAN MT3_STREE MT3_STREE MT4_STREE MT4_S	AMYS_MOUSE
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2002 2002 11993 1188 999 999 999 999 999 999	ξ
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ALIGNMENTS

Ouery Match 53.6%; Score 271; DB 1; Length 71; Best Local Similarity 50.8%; Pred. No. 5.08e-45; Matches 30; Conservative 11; Mismatches 18; Indels 0; G; 13 NPCCDAATCKLRQGAQCAEGLCCDQCRFMKKGTVCRIARGDDMDDYCNGISAGCPRNPF : :
S3.6%; SC Conservative 11 CCKLROGAQCAEGLCCDQ 1: KCEPREGEHCISGPCCRN STANDARD;

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[5]
STRUCTURE BY NMR
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DISG_TRIGA
P17496;
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                                                                                                   PROC. NATL. ACAD. SCI. U.S.A. 86:8050-8054(1989).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIB-IIIA COMPLEA. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90207217.

DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,

DEISHER T.A., BUNTING S., LAZARUS R.A.;

PROC. NATL. ACAD. SCI. U.S.A. 87.2471-2475(1990).

-!- FUNCTION: INHIBITS FIBLINGEN INTERACTION WITH PLATELET RECEPTORS

EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE

GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT

AGGREGATION. INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRIMERESUROS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       13 NPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVC-RARGDDVNDYCNGISAGCPRNPF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND COLLAGEN.
-!- THE SEQUENCE SHOWN IS THAT OF TRIGRAMIN BETA-2.
-!- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-TIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR; D35982, D35982.
                                                                                                                                                                            AND COLLAGEN.
-!- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ATTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR; A33990; A33990.
                                        SEQUENCE.
MEDLINE; 90046735.
CHAO B.H., JAKUBOMSKI J.A., SAVAGE B., PING CHOW E., MARZEC U.M.,
HARKER L.A., MARAGANORE J.M.;
HARKER L.A., MARAGANORE J.M.;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AGG-1990 (REL. 15, CREATED)
01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION
                                                                                                                                                                                                                                                                                                                                              Score 267; DB 1; Length 71; Pred. No. 5.05e-44; 9; Mismatches 18; Indels
                                                                                                                                                                                                                                              HSSF; F1/434; Ans...
PROSITE; PS00427; DISINTEGRINS; 1.
PROSOL COAGULATION; PLATELET; CELL ADHESION; VENOM. DISULFID 47. 65 BY SIMILARITY.
SITE 50 52 CELL ATTACHMENT SITE.
SPONTENCE 71 AA; 7522 MW; 320595A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                            Query Match 52.8%;
Best Local Similarity 52.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                         P17494; 1KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE=VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISB_TRIGA
P17495;
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SMITH K.J., JASBJA M., LU X., WILLIAMS J.A., HYDE E.I., TRAYER I.P.;
INT. J. PEPT. PROTEIN RES. 48:220-228(1996).

-! FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.A.,
                                                                                               01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DISINTEGRIN TRIGRAMIN GAMMA (ALBOLABRIN) (PLATELET AGGREGATION
ACTIVATION INHIBITOR).
TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE),
                                                                             10 SPANPCCDAATCKLLPGAQCGEGPCCDQCSFMKKGTICRRARGDDLDDYCNGRSAGCPRN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-T.ALBOLABRIS;
MEDLINE; 94109384.
JASEJA M., SMITH K.J., LU X., WILLIAMS J.A., TRAYER H., TRAYER I.P.,
HYDE B.I.;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND COLLAGEN.
-!- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
RTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR; A23731; A23731.
PIR; $43021; $43021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W., COOK J.J., JAMESON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A., DEISHER T.A., BUNTING S., LAZARUS R.A.; PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
                                                                                                                                                                                                                                                                                                                                                                      AND TRIMERESURUS ALBOLABRIS (WHITE-LIPPED PIT VIPER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
                                                ö
Score 266; DB 1; Length /J. Pred. No. 8.97e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILLIAMS J., RUCINSKI B., HOLT J., NIEWIAROWSKI S., BIOCHIM. BIOPHYS. ACTA 1039:81-89(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P17494; IKST.
PROSITE: PS00427; DISINTEGRINS; 1.
PROSITE: PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
BISULFID 8 16 PROBABLE.
                                                                                                                                                                                                                                             ¥
                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHAEFER W., SOSZKA T., LU
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-T.ALBOLABRIS; TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUR. J. BIOCHEM. 218:853-860(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-T.GRAMINEUS; TISSUE-VENOM; MEDLINE; 90207217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-T.ALBOLABRIS;
MEDLINE; 91242430.
ACALVETE J.J., SCHAEFER W., SOSZKI
NIEWIAROWSKI S.;
BIOCHEMISTRY 30:5225-5229(1991).
                                                                                                                                                                                                                                                                      01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQ
             Query Match 52.6%;
Best Local Similarity 48.4%;
Matches 30; Conservative
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-T.ALBOLABRIS;
MEDLINE; 97052455.
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RY 62
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P31984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 RF 71
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SEOUENCE.
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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-1- SIMILARIY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
ANTAGONISTS, G43019, G43019, G43019, G43019, P17494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
50 52 CELL ATTACHMENT SITE (POTENTIAL).
SITE
71 AA; 7637 MW; 910AF02C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN 69
                                                                                                                                                                                                                                      9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISI_CROVE STANDARD; PRT; 72 AA.
P31985;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
CROTALUS CREBERIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN VIRIDIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALLS VIRIDIS VIRIDIS (PRAIRIE RATTLESNAKE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURA, SERPEPRIES.
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                                                                                                                                   Score 258; DB 1; Length 73;
Pred. No. 8.73e-42;
11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
                                                                              CELL ATTACHMENT SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 253; DB 1; I
Pred. No. 1.51e-40;
12; Mismatches 21;
                                                                                               DA64D759 CRC32;
                                                                                                                                                                                                                                                                                                                                 71 AA.
    PROBABLE
                                        PROBABLE
                                                                                                                                                                                                                                                                                                                                   PRT;
35
59
38
66
53
7573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.8%;
Matches 29; Conservative
                                                                                                                                   Query Match 51.0%;
Best Local Similarity 50.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
    21
23
34
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                             LT 5
DISI_CROVV
P31987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RF 70
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DISULFID
DISULFID
DISULFID
DISULFID
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SEQUENCE.
                                                                                             SEQUENCE
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1D DI
AC P3
AC P3
DD O1
DD O1
DD O2
DD OC EE
COC EE
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SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZI L., ARRETEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268-1058-1055(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPEIN IIB-III. COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-III. RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; H43019; H43019.
                                                                                                                                                                                                                FACTOR AND COLLAGEN.

-- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROFEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
HSSP; P17494; 1KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 SPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN MOLOSSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS MOLOSSUS MOLOSSUS (NORTHERN BLACK-TAILED RATTLESNAKE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                       BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL).
SEQUENCE 72 AA; 7781 MW; BFE2B942 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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BROSITE; RS00427; DISINTEGRINS; 1.

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

SITE
53 CELL ATTACHMENT SITE (POTENTIAL)

CELL ATTACHMENT SITE (POTENTIAL)

CENTER 73 AA: 7880 MW; 7312E08D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 4.72e-40;
10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 252; DB 1; 1
Pred. No. 2.67e-40;
12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                          PS00427; DISINTEGRINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.8%;
larity 46.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.6%;
larity 49.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHOF
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P17494; 1KST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-VENOM;
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71 AA.

PRT;

STANDARD;

STATE REPORT OF THE PROPERTY O

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INTELLATOR MUSCLAGEN

FACTOR AND COLLAGEN

SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; A43020; A43020.
HSSP; P17494; IKST.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 66

EY SIMILARITY.
                     13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (REL. 15, CREATED)
1-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DISINTEGRIN ECHISTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
                                                                                                                                                   01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN JARARACIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N Z.R., GOULD R.J., JACOBS J.W., FRIEDMAN P.A., POLOKOFF M.A.;
BIOL. CHEM. 263:19827-19832(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90207217.
DENNIS, M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
                                                                                                                                                                                                                                BOTHROPS JARARACA (JARARACA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECHIS CARINATUS (SAW-SCALED VIPER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL ATTACHMENT SITE (POTENTIAL). 15EEAA7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 250; DB 1; Length 73;
Pred. No. 8.33e-40;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 AA.
                                                                                                                 73 AA
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AA; 7739 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 50.8%; tes 30; Conservative
                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=VENOM;
MEDLINE; 89066819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92104150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=VENOM;
                                                                                             GT 10
DISI_BOTJA
P31989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISI_ECHCA
                                                                                                                                                                                                                                                                                                              SEOUENCE
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                                                                                                                                                                                MEDLINE; 91002685.

RECINSKI B., NIEWIAROWSKI S., HOLT J.C., SOSZKA T., KNUDSEN K.A.;

R. WICHIM. BIOCHIS. ACTA 1054:257-265(1990).

R. BIOCHIM. BIOCHIS. ACTA 1054:257-265(1990).

C. EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE CLYCOPTORY IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INITIALIZA AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR AND COLLAGEN.

C. INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR AND COLLAGEN.

ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. BR SSP; P17494: 1KST.

PROSITE; PSO0427; DISINTEGRINS; 1.

RECOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

PLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

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TAM: A STATE ATTACHMENT SITE.
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NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIGL. CHEM. 268:1058(1993).
-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROFEN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
           01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISJUNEGRIN BATROXOSTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHNOPS ATROX (BARRA AMARILLA) (FER-DE-LANCE).
EUKARYOTA: METAZOÀ; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROFEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. PIR; F43019; F43019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN COTIARIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
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CELL ATTACHMENT SITE (POTENTIAL)
0D73D088 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 250; DB 1; Length 72;
Pred. No. 8.33e-40;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 250; DB 1; 1
Pred. No. 8.33e-40;
9; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P17494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOOD COAGULATION; PLATELET;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.4%;
Best Local Similarity 50.8%;
Matches 30; Conservative
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Best Local Similarity 50.00,
30; Conservative
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                                                                                                                                 LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-VENOM;
MEDLINE; 93123215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 9
DISI_BOTCO
P31988;
                                                                                                                                                                     SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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STANDARD;
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Best Local Similarity 4'
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MEDLINE; 89229063.
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MEDLINE; 88058981.
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                                                       TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE-VENOM;
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P15503;
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                                              SEQUENCE
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  SO CCC CCC RAY RESPONDE
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                                                                                                                                                                                                                                                  FEBS LETT. 309:316-320(1992).
-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
-!- FUNCTION: ON GLYCOPROTEIN IIB-IIB- COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SUBFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                CELL ADHESION; VENOM; 3D-STRUCTURE.
PYRROLIDONE CARBOXYLIC ACID (IN ALPHA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  ×.
                                                                                                                                                                                                                                                                                                AND COLLAGEN.
THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
A32029; A32029.
                         STRUCTURE BY NMR.
MEDLINE; 92104151.
COOKE R.M., CARTER B.G., MARTIN D.M.A., MURRAY-RUST P., WEIR M.P.;
EUR. J. BIOCHEM. 202:323-328(1991).
DALVIT C., WIDMER H., BOVERMANN G., BRECKENRIDGE R., METTERNICH EUR. J. BIOCHEM. 202:315-321(1991).
                                                                                                                                                            STRUCTURE BY NMR.
MEDLINE: 92089067.
CHEN Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                        MEDLINE; 92387379.
CALVETE J.J., WANG Y., MANN K., SCHAEFER W., NIEWIAROSKI
STEWART G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249; DB 1; Length 49;
Pred. No. 1.47e-39;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE.
MISSING (IN ALPHA-2 FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QCESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P., PELTON J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0A851E33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA
                                                                                                                                   SAUDEK V., ATKINSON R.A., PELTON J.T.; BIOCHEMISTRY 30:7369-7372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE
                                                                     STRUCTURE BY NMR.
MEDILINE, 92104152.
SAUDEK V., ATKINSON R.A., LEPAGE P.,
EUR. J. BIOCHEM, 202:329-338(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                        PS00427; DISINTEGRINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  FORM)
                                                                                                                                                                                                  BIOCHEMISTRY 30:11625-11636(1991)
                                                                                                                                                                                                                                                                                                                                                                                BLOOD COAGULATION; PLATELET;
MOD_RES 1 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5424 MW;
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Similarity 71.1%;
32; Conservative
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49
13
13
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26,
26,
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S29198; S29198.
ZECH; 31-OCT-93.
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Matches 32; Conser
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(REL.
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STRUCTURE BY NMR.
MEDLINE; 91308124
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P31981;
01-JUL-1993 (
01-JUL-1993 (
01-JUL-1993 (
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VARIANT
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-i- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE GLYCOPROTEIN LIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR AND COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
HSSP; P17494; 1KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NUV-1995 (REL. 32, LAST ANNOTATION UPDATE)
101-NUV-1995 (REL. 32, LAST ANNOTATION UPDATE)
101-NUT-USNOM METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) (CONTAINS:
DISINTEGRIN TRIGRAMIN ALPHA (PLATELET AGGREGATION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNAKE)
DISINTEGRIN BASILICIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS BASILICOS (MEXICAN WEST-COAST RATTLESNAKE).
EUKRAKOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A., DEISHER T.A., BUNTING S., LAZARUS R.A.; PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
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Trimersurug gramineus (indian green tree viper) (green habu s
Eugrarvota; metazoa; chordata; vertebrata; tetrapoda; reptilia;
Lepidosauria; serpentes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00427; DISINTECRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 50 52 CELL ATTACHMENT SITE (POTENTIAL).
SEQUENCE 72 AA; 7704 MW; 4B255615 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                         MEDLINE; 93123215.
SCARBOROUGH R.M., ROSE J.W., NAUCHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 245; DB 1; Length 72;
Pred. No. 1.42e-38;
13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUANG T.-F., HOLT J.C., LUKASIEWICZ H., NIEWIAROWSKI S., J. BIOL. CHEM. 262:16157-16163(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIRBY E.P., NIEWIAROWSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AA
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TISSUE-VENOM GLAND;
MEDLINE; 90332429.
MEDER M.P., JACOBSON M.A.;
NUCLEIC ACIDS RES. 18:4255-4255(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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llarity 45.2%;
Conservative
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TISSUE-VENOM;
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                                                                                                                                                                                                                                    Query Match
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POTE TO STAND THE 
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NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BJOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
-i- FUNCTION: THIS PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT ACTS IN HEMORRHAGE (BY SIMILARITY).

-I- FUNCTION: TRIGRAMN INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN INB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN INB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR AND COLLAGEN.

-!- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.

-!- SIMILARITY: HIGH, IN THE C-TERMINAL REGION, TO OTHER DISINTEGRINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 SPANPCCDAATCKLIPGAQCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCNGRSAGCPRN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (REL. 26, CREATED)
1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SHOTATION UPDATE)
DISINTEGRIN LACHESIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACHESIS MUTA MUTA (BŪSHWASTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PUTATIVE ZINC METALLOPROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRICRAMIN.
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 245; DB 1; Dred. No. 1.42e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D59DA91F CRC32;
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12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 48.4%;
Best Local Similarity 45.2%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                 EMBL; X51530; G64408; -. PIR; A29784; A29784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEPIDOSAURIA; SERPENTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                            PIR; A30065; A30065
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MEDLINE; 93123215.
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P31990;
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METAL
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NANNIZZI L., ARESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058:1058:1058:1033).
-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
      INHIBLIS AND COLLEGEN.
FACTOR AND COLLEGEN.
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIS, E43019; E43019.
HSSP: P17494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
-COLLEGEN STATE (POTENTIAL).
SITE
-COLLEGEN STATE (POTENTIAL).
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ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
BH3019; B43019; D43019.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGTVCRPARGDWNDDTCTGQSADCPRN 68
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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANOTATION UPDATE)
DISINTEGRIN CROTATROXIN/DURISSIN (PLATELET AGGREGATION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CROTALUS ÅTROX (WESTERN DIAMONDBACK RATILESNAKE), AND CROTALUS DURISSUS DURISSUS (CENTRAL AMERICAN RATILESNAKE).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA; LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, D45017, D1001717 HSSP, P17494; JKST.
PROSITE: PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                               Score 242; DB 1; Length 73;
Pred. No. 7.78e-38;
10; Mismatches 22; Indels
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Pred. No. 5.92e-33;
10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Fri Sep 25 13:16:33 1998 Job time : 8 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                     47.88;
                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 47.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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protein - protein database search, using Smith-Waterman algorithm srch_pp

MasPar time 6.66 Seconds 423.886 Million cell updates/sec Fri Sep 25 13:16:50 1998; Run on:

Tabular output not generated.

Title: Description: Perfect Score:

>PCT-US98-16719-19 (1-67) from PCTUS9816719A.pep 506 1 NSVHPCCDPVKCEPREGEHC......DYCSGIIPDCPRNRYKXXXD 67 Sequence:

PAM 150 Gap 11 Scoring table:

140555 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb16 Database:

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified

Mean 32.803; Variance 51.059; scale 0.642 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8	.75e-76	.92e-45	.22e-44	.38e-35	05e-33	.25e-32	11e-31	85e-31	85e-31	85e-31	,94e-30	94e-30	.37e-29	1.37e-29	1.37e-29	2.37e-29	.08e-29	.08e-29	2.11e-28	2.11e-28
Pred. No	1.75	6.9	1.22	1.38	2.05	3.25	5.11	8.85	8.85	8.85	7.94	7.94	1.37	1.37	1.37	2.37	7.08	7.08	2.11	2.11
Description	LEBETASE LE3 PRECURSOR	PREPRO-HALYSTATIN 2 (F	PREPRO-HALYSTATIN PREC	PREPRO-HALYSTATIN 3 (F	MEMBRANE ANCHORED META	PRO-TRIMUCIN PRECURSOR	FERTILIN ALPHA.	METALLOPROTEINASE-DISI	MDC15.	METARGIDIN PRECURSOR.	ECARIN PRECURSOR.	METALLOPROTEASE.	MELTRIN BETA, PARTIAL	FERTILIN BETA.	FERTILIN BETA.	ADAM 13.	ATROLYSIN E PRECURSOR	CELLULAR DISINTEGRIN-R	FERTILIN BETA (FRAGMEN	FERTILIN BETA.
D	098995	090221	090220	090222	042593	091505	P70505	042138	013493	013444	090495	090499	035674	028472	028478	012960	992119	060472	P78326	099965
DB	12	12	12	12	12	12	10	12	~	~	12	12	10	4	4	12	12	9	~	7
a Query Match Length	478	117	480	115	206	481	789	620	814	814	616	617	150	735	735	914	487	111	735	735
% Query Match	78.5	53.8	53.6	46.2	44.5	43.5	42.5	42.3	42.3	42.3	41.5	41.5	41.3	41.3	41.3	41.1	40.7	40.7	40.3	40.3
Score	397	272	271	234	225	220	215	214	214	214	210	210	209	209	509	208	206	206	204	204
Result No.	-	71	E	₹	ស	ø	_	∞	σ	10	11	12	13	14	15	16	17	18	19	20

3.19e-27	3.19e-27	5.49e-27	8.20e-26	8.20e-26	8.20e-26	2.41e-25	1.21e-24	2.07e-24	2.07e-24	6.03e-24	1.03e-23	1.03e-23	3.00e-23	3.00e-23	5.10e-23	5.10e-23	8.69e-23	8.69e-23	1.48e-22	4.28e-22	7.27e-22	2.09e-21	3.55e-21	3.55e-21
FERTILIN ALPHA (PH-30		FERTILIN ALPHA-II (FRA	FERTILIN ALPHA-II.	FERTILIN ALPHA-I (FRAG	FERTILIN ALPHA-I.	ADAM7.	EPIDIDYMAL APICAL PROT	PUTATIVE METALLOPROTEI	METALLOPROTEASE/DISINT	CATROCOLLASTATIN PRECU	A DISINTEGRIN AND META	FERTILIN BETA SUBUNIT.	HEMORRHAGIC TOXIN A (E	FERTILIN ALPHA PROTEIN	TMDC V (FRAGMENT).	FERTILIN ALPHA SUBUNIT	TMDC VI (FRAGMENT).	FERTILIN ALPHA-I (FRAG	EPIDIDYMAL APICAL PROT	PH-30 BETA PRECURSOR.	MELTRIN, ALPHA.	FERTILIN BETA.	METALLOPROTEASE/DISINT	PH-30 ALPHA.
060813	961072	019061	028477	019056	028476	035227	063180	010718	013443	090282	060815	028660	092043	019057	P97777	028659	P97778	019060	028475	960411	061824	063202	042595	060410
10	10	7	7	7	7	10	2	~	~	12	10	4	12	4	10	4	10	4	4	2	2	9	12	10
900	845	792	825	838	905	788	789	411	819	609	473	751	419	836	203	919	81	821	176	735	903	739	48	804
39.3	39.3	39.1	38.1	38.1	38.1	37.7	37.2		37.0	36.6	36.4	36.4	36.0	36.0	35.8	35.8	35.6	35.6	35.4	35.0	34.8	34.4	34.2	34.2
199	199	198	193	193	193	191	188	187	187	185	184	184	182	182	181	181	180	180	179	177	176	174	173	173
21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		VERTEBRATA; DEA;		8; 0; Gaps 0; ISSDCPRN 474 :: ITPDCPRN 60		
3 AA.	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	LEBETASE LE3 PRECURSOR. MACROVIDERA LEBETINA (LEVANTINE VIPER). ERRARYOTAE; MITOCHONDRIAL EUKARYOTES; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA; SCLEROGIOSSA; SERPENTES; COLUBROIDEA; VIPERIDAE; VIPERINAE; MACROVIPERA.	LILI SEQUENCE FROM N.A. TISSUE-VENOM GLAND. TISSUE-VENOM GLAND. SIGGRE, ASPOLLU A., TU A.T., SIIGUR J.; BIOCHEM. BIOPHYS. RES. COMMUN. 224:229-236(1996). EMBL, X97894; E246059; PROSITE; PSO0427; DISINTEGRINS; 1. PROSITE; PSO0427; DISINTEGRINS; 1. SIGNAL, BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM SIGNAL 194 478 POTENTIAL. CHAIN 194 478 POTENTIAL.	tch 78.5%; Score 397; DB 12; Length 478; al Similarity 76.2%; Pred. No. 1.75e-76; 48; Conservative 7; Mismatches 8; Indels 0; Gap NSGNPCCDPVTCQPRRGEHCVSGKCCRNCKFLRAGTVCKRAVGDDMDDXCTGISSDCPRN : :		7 AA. JE UPDATE) KION UPDATE)
; PRT; 478		NTINE VIPER). EUKARYOTES; MI LEROGLOSSA; SI OVIPERA.	TU A.T., SIIGUR J.; COMMUN. 224:229-236(1996) TEGRINS; 1. CON; PLATELET; CELL ADHESIC POTENTIAL. POTENTIAL. RO MW; 384418C4 CRC32;	Score 397; DB 12; Pred. No. 1.75e-76; 7; Mismatches 8 SGKCCRNCKFLRAGTVCKRAV 		; PRT; 117 AA. , CREATED) , LAST SEQUENCE UPDATE) TAST ANNOTATION UPDATE) ENT.
PRELIMINARY;	\sim \sim \sim	LEBETASE LE3 PRECURSOR. MACROVIPERA LEBETINA (LEVANTINE VIPER) EURARYOTAE; MITOCHONDRIAL EURARYOTES; LEPTDOSAURA; SQUAMATA; SCLEROGLOSSA; VIPERIDAE; VIPERINAE; MACROVIPERA.	SEQUENCE FROM N.A. TISSUE-VENOM GLAND; SIGGUR E., AASPOLLU A., TU A.T., S SIGGUR B., PAGPOLLU A., TU A.T., S BICCHEM, BIOPHYS. RES. COMMUN. 224 EMBL, X97894; E246059; SIGNAL; BLOOD COGGULATION; PLATELE SIGNAL; BLOOD COGGULATION; PLATELE SIGNAL 194 478 POTEN SEQUENCE 478 AA; 53480 MW; 384	78.5%; Similarity 76.2%; 48; Conservative NPCCDPVTCQPRRGEHCV : :		1 2 100221 PRELIMINARY; P. 200221 200221 C. 100-1096 (TREMBLREL. 01, CRE. 01-NOV-1996 (TREMBLREL. 05, LAS' DRERO-1998 (TREMBLREL. 05, LAS' PREMBLY 1098 (TREMBLELEL. 05, LAS' PREMBRY)
098995	01-FEB-1997 01-FEB-1997 01-JAN-1998	LEBETASE LE3 MACROVIPERA DENKARYOTAE; LEPIDOSAURIA	EQUENCE FROM N.A. TISSUE-VENOM GLAND; SIGGHE E., AASPOLLU A., BIOCHEM. BIOPHYS RES. EMBL; X97894; E246059; PROSITE; PSO0427; DISIR SIGNAL; BLOOD COAGULATI SIGNAL 1 1 18 CHAIN 194 478 SEQUENCE 478 AA; 533	Query Match Best Local Simi Matches 48; 415 NSGNPCC 1 INSVHPCC	475 PYK 477 11 RYK 63	0117 2 090221 090221; 090221; 01-NOV-1996 01-JAN-1998 PREPRO-HALYS
ID OF	2222	888888	RR RR RR DR CR KW KW FT SO	o a a	Db	RESULT ID Q AC Q DT 0 DT 0

Page 2

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467 QN 468
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                                                                                                                                                                                                                                                                                                                                    042593
042593;
                                                                 NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                            2 SVHPCCDPVKCEPREGEHCISGPCCRNCYFLXAGTXCKRAVGDDVDYCSGITPDCPRNR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 NPCCDAATCKLRQGAQCAEGLCCDQCRFMKKGTVCRIARGDDMDDYCNGISAGCPRNPF 478
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
FUJISAWA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
TAKEDA KENKYUSHO HO 53:39-56(1994).
EMBL; D28871; G559398; -.
PROSITE; PS00427; DISINTECRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-VENOM GLAND;
TUSSUB-VENOM GLAND;
TUSSUB-VENOM GLAND;
TAKEDA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA 2.I.;
TAKEDA KENKUDO HO 53:39-56(1994).
EMBL; D28870; G469190; -..
PROSITE; PSO0427; DISINTEGRINS; 1.
SIGNAL; BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUJISAWA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
TAKEDA KENKYUSHO HO 53:39-56(1994).
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EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
  EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 271; DB 12; Length 480;
Pred. No. 1.22e-44;
11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTII
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE
                                                                                                                                                                                                                                                                                          Query Match 53.8%; Score 272; DB 12; Length 11 Best Local Similarity 49.2%; Pred. No. 6.92e-45; Matches 30; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPRO-HALYSTATIN 3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPRO-HALYSTATIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AA; 53619 MW; 68983596 CRC32;
                                                                                                                                                                                                                                             SEQUENCE 117 AA; 12686 MW; 15139DFC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 3
090220
090220;
                                                                                                                                                                                                                        NON TER
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNORATION UPDATE)
MEMBRANE ANCHORED METALLOPROTEASE, DISINTEGRIN, CYSTEINE-RICH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 SCCDPTSCKLRENGECLTGLCCKDCKLLPKGTLCRMPKTECDLAEYCDGASNHCPLDMYK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMUDIUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 PANPCCDAATCKLRPGAQCAEGLCCDQCRFIKAGTVCRRARGDWNDNTCTGQSADCPRN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-SNAKE VENOM GLAND;
TSAI J.H., WANG Y.M., LEE Y.H.;
BIOCHIM. BIOPHYS. ACTA 1200:337-340(1994).
EMBL, 77089; G467704; -
PROSITE; PSO0427; DISINTEGRINS; 1.
SIGNAL; METALLOPROTEASE; BLOOD COAGULATION; PLATELET; CELL ADHESION;
                                                                                                                                                                                                                                                                               2 SVHPCCDPVKCEPREGEHCISGPCCRNCYFLXAGIXCKRAVGDDVDDYCSGITPDCPRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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091505;

01-NOV-1996 (TREMBLREL, 01, CREATED)

01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)

01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)

PRO-TRIMUCIN PRECURSOR.

TRIMERSURUS MUCROSQUANATUS (TAIWAN HABU).

EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
                                                                                                                                                Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-TESTIS,
TISSUE-TESTIS,
TISSUE-TESTIS,
TISSUE-TESTIS,
TISSUE F.M., KRAETZSCHWAR J, GAYKO U., CAI H., WESKAMP
LEIBOW L., MYLES D.G., NUCCITELLI R., BLOBEL C.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U78185; G2231331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 225; DB 12; Length 70
Pred. No. 2.05e-33;
14; Mismatches 23; Indels
                                                                                                                                              Score 234; DB 12; Length 11
Pred. No. 1.38e-35;
10; Mismatches 20; Indels
EMBL; D28871; G559299; -. PROSITE; PS00427; DISINTEGRINS; 1. BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 220; DB 12;
Pred. No. 3.25e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTEGRIN; PROTEASE; METALLOPROTEASE.
SEQUENCE 706 AA; 79275 MW; 8992584A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-TRIMUCIN.
23A332F0 CRC32;
                                                                                                  SEQUENCE 115 AA; 12389 MW; C10C6FAF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      706 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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481 PRC
54079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.18;
                                                                                                                                                Query Match
Best Local Similarity 49.2%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
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Matches

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442 DCVDPCCDSLTCQLRPGAQCASDGPCCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQCP 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 DCVDPCCDSLICQLRPGAQCASDGPCCQNCQLRPSGWQCRPIRGDCDLPEFCPGDSSQCP 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + HPCCDPVKCEPREGEHCISGPCCRNCYFLXAGIXCKRAVGD-DVDDYCSGITPDCPRNRY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOCIS.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01344;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
METARGIDIN PRECURSOR.
HOMO SAPIENS (HDANN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 214; DB 2; Length 814;
Pred. No. 8.85e-31;
18; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 214; DB 2; Length 814;
Pred. No. 8.85e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches 17; Indels
                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METARGIDIN.
9767B2E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                   814 AA; 87716 MW; A2ABFE2F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              814 AA.
                                                                                                                                              814 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOBEL C.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
KRASTSZCHMAR J.R., LUM L., BLOBEL C
J. BIOL. CHEM. 271:4593-4596(1996).
EMBL; U41767; G1235674; -.
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                      ROSS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 814 N
814 AA; 87686 MW;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-UNBALLICAL VEIN;
MEDLINE; 97192141.
HERREN B., RAINES E.W., ROSS
FASEB J. 11:173-180(1997).
EMBL; U46005; G1335972; -
SEQUENCE 814 AA; 87716 MW
                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.3%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Conservative
                                              487 QRN 489
                                                                               KXK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 PD 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                           013493;
                                                                                                                            T 9
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 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 HPCCEPT-CTLKVGAQCSEGLCCYKCTFKKKGTLCRPAEDVCDLPEYCNGITGECPANSY 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 NPCCDAATCKLTPGSQCADGVCCDQCRFTRAGTECRQAKDDCDMADLCTGQSAECPTDRF 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                             421 NPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRCTGQSADCPRN 477
                                                             9
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DE ARRUJO H.S., OWNBY C.L.;

DE BARUJO H.S., OWNBY C.L.;

SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; U86634; G2231613; -..

PROSITE; PS00427; DISINTEGRINS; 1.

INTEGRIN; HYDROLASE; BLOOD COAGULATION; PLATELET; CELL ADHESION;
                                                   01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
METALLOPROTEINASE-DISINTEGRIN-LIKE PROTEIN (EC 3.4.24.1).
AGKISTRADON CONTORTRIX LATICINCTUS.
EUKARYOTA; METALCA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
                                                                                                                                                                                                      FERTILIN ALPHA.
RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 789;
 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                  HALL L.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y08616; E274094; -.
SPERM: TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
BEARAUJO H.S., OWNBY C.L.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 215; DB 10;
Pred. No. 5.11e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 AA; 69512 MW; OFE0D01A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE; 95314311.
DE ARAUJO H.S., OWNBY C.L.;
ARCH. BIOCHEM. BIOPHYS. 320:141-148(1995).
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY; TISSUE-TESTIS;
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                        RESULT 7
1D P70505;
DT 01-FEB-1997 (TREMBLREL. 02, CR DT 01-FEB-1997 (TREMBLREL. 02, LA DT 01-FEB-1997 (TREMBLREL. 02, LA DE FERTILIN ALPHA.

S RATTLIN ALPHA.
OS RATTLIN NORVEGICUS (RATT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.5%;
Best Local Similarity 44.3%;
Matches 27; Conservative
Conservative
 28;
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K 63
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042138;
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Matches

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MGI:105377
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SEQUENCE
  LT 13
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035674;
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Q28472
Q28472;
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TISSUE-VENOM GLAND;
MEDLINE; 95010025.
PAINE M.J.I., MOURA-DA-SILVA A.M., THEAKSTON R.D.G., CRAMPTON J.M.;
PAINE M.J.I., MOURA-DA-SILVA A.M., THEAKSTON R.D.G., CRAMPTON J.M.;
EUR. J. BIOCHEM. 224:4813-488(1994).
EMBL; X78970; G763093; --
PROSITE, PSO0427; DISINTERRINS; 1.
PROTEASE; METALLOPROTEASE; BLOOD COAGULATION; PLATELET; CELL ADHESION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 NPCCDAATCKLKPGAECGNGECCDKCKIRKAGTECRPARDDCDVAEHCTGQSAECPRNEF 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 210; DB 12; Length 616;
Pred. No. 7.94e-30;
15; Mismatches 24; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 NPCCNATTCKLTPGSQCADGECCNQCRFRPARTECRRKIDDCDVPEYCTGQSGECPLDVF 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPIILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE; VIPERINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 HPCCDPVKCEPREGEHCISGPCCRNCYFLXAGTXCKRAVGD-DVDDYCSGIIPDCPRNRY 62
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-VENOMOUS GLAND;
MEDLINE; 95121760.
NISHIDA S., FUJITA T., KOHNO N., ATODA H., MORITA T., TAKEYA H.,
KIDO I., PAINE M.J., KAWABATA S., IWANAGA S.;
BICCHEMISTRY 34:1771-1778(1995).
                                                                                                                                            ECHIS CARINATUS (SAW-SCALED VIPER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.5%; Score 210; DB 12; Length 617; 35.4%; Pred. No. 7.94e-30; vative 14; Mismatches 27; Indels 1
                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
ECARIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
ECARIN.
: DE2FC9AA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69310 MW; D929D8D3 CRC32;
                      616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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191 616 EX
616 AA; 69462 MW;
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01,
                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.5%;
Best Local Similarity 38.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           larity 35.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617
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617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
ses 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECHIS PYRAMIDUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 QRNGQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 QRNGQ 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 KXKXD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 KXKXD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
LT 11
090495
090495;
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Q90499
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RESULT
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Score 209; DB 10; Length 150;
Pred. No. 1.37e-29;
17; Mismatches 19; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 CCDTATCRFKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGTSASCPENHF 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

RAMARAO C.S., MYLES D.G., WHITE J.M., PRIMAKOFF P.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. U33959; G998340; -.
PROSITE: PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SEQUENCE 735 AA; 82372 MW; 8E68BAC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 15
PRELIMINARY; PRT; 735 AA.
028478
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JNN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PERTILIN BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
FERTILLIN BETA.
                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
MELTRIN BETA, PARTIAL CDS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150
16395 MW; E8B6AAFC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                735 AA
                                                                                        01-JAN-1998 (TREMBLREL. 05, CREATED)
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local Similarity 36.2%;
Matches 21; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.3%;
Best Local Similarity 38.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 96026308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
1D 02
AC 022
AC 021
DT 011
DT 011
DT 010
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MEDLINE; 95260313.
PERRY A.C.F., GICHUHI P.M., JONES R., HALL L.;
BICCHEM. J. 307:843-850(1995).
EMBL; X77653; G794077; ---
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM. SEQUENCE 735 AA; 82358 MW; F31BBC91 CRC32;
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Carch completed: Fri Sep 25 13:17:04 1998 Job time : 14 secs.

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protein - protein database search, using Smith-Waterman algorithm srch_pp

Fri Sep 25 13:20:29 1998; MasPar time 4.08 Seconds 412.235 Million cell updates/sec Run on:

Tabular output not generated.

1 NSVHPCCDPVKCEPREGEHC.........DYCSGITPDCPRNRYKXKXD 67 >PCT-US98-16719-19 (1-67) from PCTUS9816719A.pep 63 Title: Description: Perfect Score: Sequence:

Scoring table:

69111 seqs, 25083644 residues TABLE unitprotable Gap 60 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 2.933; Variance 0.342; scale 8.579 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.75e-05	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00
Description	DISINTEGRIN ECHISTATIN	DISINTEGRIN BATROXOSTA	DISINTEGRIN VIRIDIN (P	DISINTEGRIN CEREBERIN	DISINTEGRIN COTIARIN (DISINTEGRIN JARARACIN	DISINTEGRIN MOLOSSIN (PHOTOSYSTEM I REACTION	PHOSPHATIDYLINOSITOL (GRAVIN (FRAGMENT).	MALONYL COA-ACYL CARRI	SRG-3 PROTEIN.	HEMIN TRANSPORT PROTEI	FERREDOXIN NADP REDUC	ATP-DEPENDENT CLP PROT	FERREDOXIN NADP REDUC	SUCROSE-6-PHOSPHATE HY	NEURAMINIDASE (EC 3.2.	AMIDASE (EC 3.5.1.4).	COBYRIC ACID SYNTHASE.	HYPOTHETICAL 66.3 KD P	PUTATIVE DIHYDROXYACET	HYPOTHETICAL 68.3 KD P
Ð	DISI_ECHCA	DISI_BOTAT	DISI_CROVV	DISI_CROVE	DISI_BOTCO	DISI_BOTJA	DISI_CROMM	PSAN_ARATH	PPI2_MOUSE	GRAV_HUMAN	FABD_BACSU	SRG3_CAEEL	HMUS_YERPE	FENR_ANASO	CLPX_AZOVI	FENR ANAVA	SCRB_SALTY	NRAM_IATOK	AMID_PSECL	CBIP_SALTY	YHA2_EIKCO	DHAK_YEAST	YG48_YEAST
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Query Match	12.7	9.5	9.5	9,5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5
Score	8	9	φ	Q	ø	9	9	ø	9	9	φ	φ	φ	Q	9	ø	9	Q	ø	9	9	9	9
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P100_HSV6U	RPB1_ARATH	RPBO_ARATH	YFIH_STRCO	YP73_GVCL	YYBA_BACSU	YOL6_CAEEL	YPEV_LACDL	YWFC_BACSU	YIT6_YEAST	Y022_CAEEL	YO42_CAEEL	YF06_METJA	YOPH_YERPS	YMV5_YEAST	YPT4_PSEAE	YES_XENLA	YIDU_ECOLI	YT32_CAEEL	YN18_YEAST	YNF4_YEAST
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ALIGNMENTS

AA.	(REL. 15, CREATED) (REL. 28, LAST SEQUENCE UPDATE)	(TE) (ON ACTIVATION INHIBITOR)		TETRAPODA: REPTILIA:						FRIEDMAN P.A., POLOKOFF M.A.;						RI M.T., NAPIER M.A.,		(1990).				BRECKENRIDGE R., METTERNICH R.					MURRAY-RUST P., WEIR M.P.;					N. d. T.;									
49 A	DATE	OPD2		4	ì					EDM						LIP		247				ECKE										PELTON									
PRT;	TED) SEQUENCE UP	ANNOTATION ATELET AGGRE	, , , ,	D VIPEK). TA: VERTEBRA						BS J.W., FRI	9832(1988).					PITTI R.M., LIPARI M.T.,	LAZARUS R.A.	U.S.A. 87:2471-2475(1990).					21(1991).				ARTIN D.M.A.	28(1991).					38(1991).				PELTON J.T.;				
STANDARD;	IL. 15, CREAIL. 28, LAST	IL. 31, LAST HISTATIN (PL	The Comments of the Comments o	CHORDA	ERPENTES.				119.	R.J., JACO	T-/786T:697				117.	ENZEL W.J.,	SUNTING S.,	ND. SCI. U.S		Æ.	.50.	IT C., WIDMER H., BOVERMANN G.,	4. 202:315-3		IR.	151.	RIER B.G., M	4. 202:323-3		Æ.			4. 202:329-338(1991).		Æ.	124.	INSON R.A.,):7369-7372(윥.	. 190
T 1 DISI_ECHCA	P1/34/; O1-AUG-1990 (RE O1-FEB-1994 (RE		(CARINATIN).	ECHIS CAKINATUS (SAM-SCALED VIPEK). EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA:	LEPIDOSAURIA: SERPENTES.	[1]	SEQUENCE.	TISSUE-VENOM;	MEDLINE; 89066819.	GAN Z.R., GOULD R.J., JACOBS J.W., FR	J. BIOL. CHEM.	[2]	SEQUENCE.	TISSUE=VENOM;	MEDLINE; 90207217.	DENNIS M.S., HENZEL W.J., PITTI R.M.,	DEISHER T.A., E	PROC. NATL. ACAD. SCI.	[3]	STRUCTURE BY NMR.	MEDLINE; 921041	DALVIT C., WIDMER H.,	EUR. J. BIOCHEN	[4]		MEDLINE; 92104151.	COOKE R.M., CARTER B.G., MARTIN D.M.A.,	EUR. J. BIOCHEN	[2]	STRUCTURE BY NMR.	MEDLINE; 92104152.	SAUDEK V., ATKI	EUR. J. BIOCHEM.	[9]	STRUCTURE BY NMR.	MEDLINE; 91308124.	SAUDEK V., ATKI	BIOCHEMISTRY 30:7369-7372(1991).	[7]	STRUCTURE BY NMR	MEDLINE; 92089067
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RUCINSKI B., NIEMIAROMSKI S., HOLT J.C., SOSZKA T., KNUDSEN K.A.;
BICCHIM. BIOPHYS. ACTA 1054:257-262(1990).
FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS FERRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBITS. AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN BATROXOSTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS ATROX (BARBA AMARILLA) (FER-DE-LANCE).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                   INHIBIT
                                                                                                                                                                                                         RECEPTORS
ING TO THE
                                                                                                                                                                        FEBS LETT. 309:316-320(1992).
-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORE EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACI BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIA AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                          153. -CT-93. PSINTEGRINS; 1. PSO0427; DISINTEGRINS; 1. PSO0427; DISINTEGRINS; 1. PYRROLIDONE CARBOXYLIC ACID (IN ALPHA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. PIR; S13168; S13168.
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THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
SIMILARITY: BELONG TO THE FAMILY OF GPILB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
A32029, A32029.
Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL G.,
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                                                                                                                                   SCHAEFER W., NIEWIAROSKI S.,
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MISSING (IN ALPHA-2 FORM).
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BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM
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                                          BIOCHEMISTRY 30:11625-11636(1991)
                                                                                                         MEDLINE; 92387379.
CALVETE J.J., WANG Y., MANN K.,
STEWART G.J.;
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A SCARBOROGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
A NANNIZZI L., AREFERDA A., CAMPBELL A.M., CHARO I.F.;
A. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INHIBITS FIBRINGGEN INTERACTION WITH PLATELET RECEPTORS
C EXPRESSED ON GLYCOPPOTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIBA RECEPTOR ON THE PLATELET SURFACE AND
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 MEDLINE; 9312315.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARRESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-i- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
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 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN CEREBERIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS VIRIDIS CEREBERUS (ASTZONA BLACK RATTLESSAKE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN VIRIDIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALLY VIRIDIS VIRIDIS (PRAIRIE RATILESNAKE).
EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
 PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 50 52 CELL ATTACHMENT SITE (POTENTIAL)
SEQUENCE 71 AA; 7637 MW; 910AF02C CRC32;
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 0; Indels
 Length 71;
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CELL ATTACHMENT SITE.
A73CFB7E CRC32;
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d. No. 1.22e+00;
Mismatches 0;
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1. No. 1.22e+00;
Mismatches 0
 71 AA.
 72 AA.
 Score 6;
Pred. No.
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7602 MW;
 Query Match 9.5%;
Best Local Similarity 100.0%;
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 Local Similarity 100.0%;
les 6; Conservative
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 LEPIDOSAURIA; SERPENTES.
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71 AA;
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 TISSUE-VENOM;
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 RESULT 3
1D DISI_CROVV
AC P31987;
DT 01-JUL-1993
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DE DISINTEGRIN
OC CTALUS VIF
CC LEPIDOSAURIA;
RN (1)
RN (1)
RN (2)
RC SCARBOROCH
RA SCARBOROCH
RA SCARBOROCH
RA SCARBOROCH
RA SCARBOROCH
RA SCARBOROCH
RA SCARBOROCH
CC TISSUE-TENOV
CC EXPRESSE
CC GLYCOPRC
CC INHIBITS
CC TRACTOR A
CC TRACTO
 DCPRNR
 DCPRNR
 LT 4
DISI_CROVE
P31985;
 01-JUL-1993
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61
 65 DCPRNR 70
 56 DCPRNR 61
 65 DCPRNR 70
 SEQUENCE.
TISSUE-VENOM;
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56 DCPRNR
 T 7
DISI_CROMM
 SEQUENCE
 Query Match
 P31984;
 Best Loca
Matches
 Matches
 RESULT
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 INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 INTELLS CONTROLLED IN COLLEGEN.
FACTOR AND COLLEGEN.
-- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR: 843020, 843020.
HSSP: PA3020, 143020.
HSSP: PA3020, 143020.
HSSP: PA3020, 150000.
HSSP: PA3020, 150000.
HSSP: PA3020, 150000.
HSSP: PA3020, 160000.
HSSP: PA3020000.
HSSP: PA3020000.
HSSP: PA3020000.
HSSP: PA3020000.
HSSP: PA3020000.
HS
 FACTOR AND COLLAGEN.
--- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; F43019; F43019.
 Gaps
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN JARARACIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-STRINGERIN COTIARIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS COTIARA (COTIRARA).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 HSSP, P17494; IKST.
HSSP, P17494; IKST.
PROSTIE: PS00427; DISINIEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 66 BY SIMILARITY.
51 53 CELL ATTACHMENT SITE (POTENTIAL).
7709 MW; OD73D088 CRC32;
 BOTHROPS JARARACA (JARÀRACA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
 ö
 Score 6; DB 1; Length 72;
Pred. No. 1.22e+00;
0; Mismatches 0; Indels
 0; Indels
 Score 6; DB 1; Length 72;
Pred. No. 1.22e+00;
0; Mismatches 0; Indel
 73 A.A.
 72 AA.
 PRT;
 PRT;
 Best Local Similarity 100.0%;
Matches 6; Control 100.0%;
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 STANDARD;
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 DCPRNR 70
 65 DCPRNR 70
 61
 DCPRNR 61
 LT 6
DISI_BOTJA
P31989;
01-JUL-1993 (
 DCPRNR
 DISI_BOTCO
P31988;
 (1)
SEQUENCE.
 SEQUENCE
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MEDLINE; 9123215.

CARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., AREPETEN A., CAMPBELL A.M., CHARO I.F.;
NANNIZZI L., AREPETEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268-1058-105931.

-I- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
C. PRYPESSED ON GLYCOPROPEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE GLYCOPROPEIN IIB-IIIA ECEPTOR ON THE PLATELET SURFACE AND INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
C. FACTOR AND COLLAGEN.
C. SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANT-GONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
RISSP; P17494; IKST.
 ö
 ö
 SCREBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. Z68:1058-1065(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROFEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGRREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 FACTOR AND COLLAGEN.
--- SMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; #43019; #43019.
 Gaps
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN MOLOSSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS MOLOSSUS MOLOSSUS (NORTHERN BLACK-TAILED RATLESNAKE).
EUKARYOTA: METAZOA; CHORDATA; VENTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA, SERRENTES.
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 ö
 CELL ATTACHMENT SITE (POTENTIAL) 15EEAA7A CRC32;
 BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL)
SEQUENCE 73 AA; 7880 MW; 7312E08D CRC32;
 0; Indels
 0; Indels
 Score 6; DB 1; Length 73;
Pred. No. 1.22e+00;
0; Mismatches 0; Indel.
 Length 73;
 DB 1; Le
1.22e+00;
 171 AA.
 73 AA.
 0; Mismatches
 Score 6;
Pred. No.
 Score 6;
Pred. No.
 PRT;
 PRT;
 HSSP; P17494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
 PSAN_ARATH STANDARD;
P49107;
01-FEB-1996 (REL. 33, CREATED)
 73 AA; 7739 MW;
 Match 9.5%;
Local Similarity 100.0%;
les 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
 Conservative
 STANDARD;
 MEDLINE; 93123215.
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32,
32,
 (REL.
(REL.
(REL.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=168;
MEDLINE; 96326321.
 GRAVIN (FRAGMENT)
 225 GDDVDD 230
 111111
43 GDDVDD 48
 80 SGITPD 85
 26
 SRG3_CAEEL
P46572;
01-NOV-1995 (
01-NOV-1995 (
01-OCT-1996 (
 51 SGITPD
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SEQUENCE
 Query Match
 Matches
 FABD.
 Matches
 RESULT
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 STRAIN-SWISS;
GEIJTENBEEK T.B.H., DER HELM H.A., SNOEK G.T., WIRTZ K.W.A.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CATALYZES THE TRANSFER OF PTDINS AND PHOSPHATIDYLCHOLINE BETWEEN MEMBRANES.
 Gaps
 Gaps
 SEQUENCE FROM N.A.
SERVIKE P.C., FERL R.J.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: MAY FUNCTION IN MEDIATING THE BINDING OF THE ANTENNA COMPLEXES TO THE PSI REACTION CENTRE AND CORE ANTENNA.
-!- SUBCELLULAR LOCATION: ON THE LUMENAL SURFACE OF THE THYLAKOID
 CHLOROPLAST (BY SIMILARITY).
PHOTOSYSTEM I REACTION CENTRE SUBUNIT
 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
 ö
 ö
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N).
 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
 EMBL; U32176; G1237124; -.
PHOTOSYSTEM I; PHOTOSYNTHESIS; CHLOROPLAST; TRANSIT PEPTIDE;
THYLAKOID MEMBRANE.
 01-OCT-1996 (REL. 34, CREATED)
1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
PHOSPHATIDYLINOSITOL (PIDINS) TRANSFER PROTEIN BETA ISOFORM
 Score 6; DB 1; Length 270;
Pred. No. 1.22e+00;
0; Mismatches 0; Indels
 Score 6; DB 1; Length 171;
Pred. No. 1.22e+00;
0; Mismatches 0; Indels
 0; Indels
 BY SIMILARITY.
ED691649 CRC32;
 E881C584 CRC32;
 (REL. 28, CREATED)
(REL. 28, LAST SEQUENCE UPDATE)
(REL. 29, LAST ANNOTATION UPDATE)
 270 AA.
 306 AA.
 -!- SIMILARITY: TO PSAN FROM OTHER PLANTS.
 -!- SUBCELLUIAR LOCATION: CYTOPLASMIC.
EMBL; U46934; G1184995; --
LIPID-BINDING; TRANSPORT.
INIT_MET
 PRT;
 PRT;
 PSAN
 270 AA; 31356 MW;
 171 AA; 18429 MW;
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 STANDARD;
 STANDARD;
 (PIDINSTP) (PI-TP-BETA).
 171
 86
 PITPNB.
MUS MUSCULUS (MOUSE)
 SEQUENCE FROM N.A.
 87
 183 TPDCPR 188
 59
 53 VGDDVD 58
 MEMBRANE.
 TPDCPR
 01-FEB-1994
01-FEB-1994
01-JUN-1994
 LT 9
PPI2_MOUSE
P53811;
 LT 10
GRAV_HUMAN
Q02952;
 INIT_MET
SEQUENCE
 SEQUENCE
 TRANSIT
 CHAIN
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 BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 Gaps
 Gaps
 FABD_BACSU STANDARD; PRT; 318 AA. 171019; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 01-NOV-1997 (REL. 35, LAST ANDOTATION UPDATE) 01-NOV-1997 (REL. 35, LAST ANDOTATE) 01-NOV
 - COA
 TISSUE-UMBILICAL VEIN ENDOTHELLAL CELLS;
MEDLINE; 92395179.
GORDON T., GROVE B., LOFTUS J.C., O'TOOLE T.E., MCMILLAN R.,
LINDSTROM J., CINSBERG M.H.;
J. CLIN. INVEST. 90:992-999(1992).
-I. FUNCTION: IT IS A COMPONENT OF THE CORTICAL CYTOSKELETON.
-I. SUBCELLULAR LOCATION: CYTOPLASMIC.
-I. DISEASE: ANTIBODIES TO GRAVIN ARE PRODUCED BY PATIENTS WITH
MYSTHENIA GRAVIS (MG).
EMBL; M96122; G183616; -.
PIR; A43922; A43922.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
 ö
 ö
 MORRIDONI H.R., DE MENDOZA D., CRONAN J.E. JR.;
J. BACTERIOL. 178:4794-4800(1996).
-!- CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN]
 + MALONIT-(ACTL-CARRIER PROTEIN).
--- STATHWAY: FATTY ACID BIOSYNTHESIS.
--- SIMILARITY: SIGNIFICANT, TO SEVERAL OTHER PROTEINS WITH TRANSACYLASE ACTIVITY.
EMBL, U59433; G150420; ---
SUBTILIST; BG11836; FABD.
FATTY ACID BIOSYNTHESIS; TRANSFERASE.
ACT_SITE 91 91 BY SIMILARITY.
SEQUENCE 318 AA; 34394 MW; 29566D74 CRC32;
 0; Indels
 0; Indels
 Length 306;
 Score 6; DB 1; Length 318;
Pred. No. 1.22e+00;
 Score 6; DB 1; Le
Pred. No. 1.22e+00;
 306 AA; 33074 MW; 3FFBC133 CRC32;
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 Mismatches
 0; Mismatches
 332 AA
 PRT;
 Match 9.5%;
Local Similarity 100.0%;
 Query Match
Best Local Similarity 100.0%;
 6: Conservative
 6; Conservative
 STANDARD;
 ANTIGEN; CYTOSKELETON.
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224 GDDVDD 229
 43 GDDVDD 48
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 NP_BIND
CONFLICT
SEQUENCE
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 PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
 SEQUENCE FROM N.A.

STRAIN=KIM6+;
HORNING J.M., JONES H.A., BERTOLINO V.J., PERRY R.D.;
HORNING J.M., JONES H.A., BERTOLINO V.J., PERRY R.D.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR HEMIN.
-!- SIMILARITY: STRONG, TO Y.ENTEROCOLITICA HEMS.
-!- SIMILARITY: STRONG, TO Y.ENTEROCOLITICA HEMS.
-!- SIMILARITY: STRONG, TO Y.ENTEROCOLITICA HEMS.
-!- SIMILARITY: TRANSPORT.
SEQUENCE 343 AA; 38859 MW; FFC2520E CRC32;
 SUBMITTED (MAY-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE SRG FAMILY OF C.ELEGANS RECEPTOR-LIKE
 Gaps
 Gaps
SRG-3 PROTEIN.
SRG-3 OR C18F10.6.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 ö
 ö
 0; Indels
 Score 6; DB 1; Length 343; Pred. No. 1.22e+00;
 0; Indels
 6; DB 1; Length 332;
No. 1.22e+00;
 FENR_ANASO STANDARD; PRT; 440 AA. P21890; 01-MAY-1991 (REL. 18, CREATED) 01-007-1994 (REL. 30, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) FERREDOXIN--NADP REDUCTASE (EC 1.18.1.2) (FNR).
 POTENTIAL.
DB0C6C73 CRC32;
 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HEMIN TRANSPORT PROTEIN HMUS.
 Mismatches
 343 AA.
 Mismatches
 POTENTIAL. POTENTIAL.
 POTENTIAL. POTENTIAL.
 POTENTIAL
 POTENTIAL
 PRT;
 Score Pred.
 EMBL; U00049; G1216304; -. WORMPEP; C18F10.6; CE02491.
TRANSMEMBRANE; MULTIGENE FAMILY
 38886 MW;
 9.5%;
Local Similarity 100.0%;
les 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 STANDARD;
 43
92
121
164
204
251
 231
263
332 AA;
 [1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
LATREILLE P.,
 YERSINIA PESTIS.
 212 RAVGDD 217
 RAVGDD 45
 18 EHCISG 23
 4 EHCISG 9
 PROTEINS.
 LT 13
HMUS_YERPE
Q56990;
 TRANSMEM
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 TRANSMEM
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C -1 - COFACTOR: FAD FLAVOPROTEIN.

-1 - SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR ANCHORED TO THE THYLAKOID-BOUND PHYCOBILISOMES.

-1 - SIMILARITY: WITH OTHER SPECIES FNR.

-1 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER PROTEIN CPCD.

-2 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER EMBL: X72394; G311533; -...

-3 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G311533; -...

-4 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31251; -...

-5 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G311533; -...

-6 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-6 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-6 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-6 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-6 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-7 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-7 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-7 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-7 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-1 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-1 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31153; -...

-1 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G315150; -...

-1 - SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER FRHS: X72394; G31234; G31234; -...

-1 - SIMILARITY: X72394; G31153; -...

-1 - SIMILARITY: X72394; G31153; -...

-1 - SIMILARITY: X72394; G31153; -...

-1 - SIMILARITY: X72394;
 Gaps
 1 80 CPCD-LIKE.
288 306 NADD (RIBOSE PART) (BY SIMILARITY).
180 I -> L (IN REF. 3).
440 AA, 48865 MW; 9F8578CF CRC32;
 AZOTOBACTER VINELANDII.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
AZOTOBACTERIACEAE.
 MEDLINE; 97045988.

SERRE L., VELLIEUX F.M.D., MEDINA M., GOMEZ-MORENO C.,
SERRE L., VELLIEUX F.M.D., MEDINA M.,
GOMEZ-MORENO C.,
J. MOL. BIOL. 263:20-39(1996).

-!- CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) - OXIDIZED FERREDOXIN + NADP(+)
 ;
0
 OXIDOREDUCTASE; FLAVOPROTEIN; NADP; FAD; THYLAKOID MEMBRANE;
PHYCOBILISOME; 3D-STRUCTURE.
 SEQUENCE FROM N.A.
MEDLINE; 89123097.
JACOBSON M.R., BRIGLE K.E., BENNETT L.T., SETTERQUIST R.A.,
WILSON M.S., CASH V.L., BEYNON J., NEWTON W.E., DEAN D.R.;
 SEQUENCE OF 152-183.
STRAIN-1403.46;
MADLINE; 88132819.
SANCHO J., PELEATO M.L., GOMEZ-MORENO C., EDMONDSON D.E.;
ARCH. BIOCHEM. BIOPHYS. 260:200-207(1988).
 Score 6; DB 1; Length 440;
Pred. No. 1.22e+00;
0; Mismatches 0; Indels
 CLPX_AZOVI STANDARD; PRT; 440 AA.
P33683;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX.
 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
ANABAENA SP. (STRAIN PCC 7119).
PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
 MEDLINE; 91088322.
FILLAT M.F., BAKKER H.A.C., WEISBEEK P.J.;
NUCLEIC ACIDS RES. 18:7161-7161(1990).
 SEQUENCE FROM N.A.
MEDLINE, 9344523.
FILLIAT M.F., FLORES E., GOMEZ-MORENO C.;
PLANT MOL. BIOL. 22:725-729(1993).
 SEQUENCE OF 137-440 FROM N.A.
 Query Match
Best Local Similarity 100.0%;
 Conservative
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RL J. BACTERIOL. 171:1017-1027(1989).

RN [2]
RP SIMILARITY TO CLPX.

RA GOTTESMAN S., CLARK W.P., DE CRECY-LAGARD V., MAURIZI M.R.;

R. GOTTESMAN S., CLARK W.P., DE CRECY-LAGARD V., MAURIZI M.R.;

R. J. BIOL. CHEM. 288:122618-22626.

C. PROTEASE. IT DIRECTS THE PROTEASE TO SPECIFIC SUBSTRATES (BY STAILLARITY).

C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FR SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONG TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

FY C. SIMILARITY: BELONGS TO THE CLPX SUBFAMILY OF CHAPERONE.

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Search completed: Fri Sep 25 13:20:38 1998 Job time : 9 secs.

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protein - protein database search, using Smith-Waterman algorithm srch\_pp

Fri Sep 25 13:20:56 1998; MasPar time 8.52 Seconds 331.078 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-19 (1-67) from PCTUS9816719A.pep 63

1 NSVHPCCDPVKCEPREGEHC......DYCSGITPDCPRNRYKXXXD Description: Perfect Score: Sequence:

67

Scoring table:

TABLE unitprotable Gap 60

140555 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl6
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 2.816; Variance 0.405; scale 6.957 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| No. Score Match Length DB   ID   Description   Pred. No.     13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |               |       | ď       |        |    |        |                        |         |
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| 1 13 20.6 478 12 098995 LEBETASE LE3 PRECURSOR 2 6 9.5 141 11 080927 TRANSFORMING PROTEIN E 6 9.5 146 9 050021 UZ266C.  4 6 9.5 14 3 018938 HYPOTHETICAL PROTEIN D 083895 ORF UL133.  5 6 9.5 257 11 068385 ORF UL133.  6 9.5 37 10 068385 ORF UL133.  7 9 033292 DEHYDROGERASE.  8 6 9.5 317 9 034463 MALONYL COA-ACYL CARRI D 06873 HYPOTHETICAL 34.9 KD P DHC (FRAGMENT).  10 6 9.5 453 1 005873 HYPOTHETICAL 34.9 KD P DHC (FRAGMENT).  11 6 9.5 453 1 005873 TOLUBEN TO KNUNENI D 065979 SIMILARITY TO KNUN | Result<br>No. | Score | Query   | Length | DB | D      | Description            |         |
| 6 9.5 141 11 Q80927 TRANSFORMING PROTEIN E 9.5 146 9 020021 U2266C.  6 9.5 14 9 020021 U2266C.  6 9.5 257 11 Q68385 ORF UL133.  6 9.5 27 12 Q68385 ORF UL133.  6 9.5 37 9 033292 DEHYDROGENAG.  6 9.5 317 9 034463 MALONIL COA-ACYL CARRI E 9.5 317 9 005873 HYDOTHETICAL 34.9 KD POGS 9.5 310 9 005873 HYDOTHETICAL 34.9 KD POGS 9.5 453 1 Q05979 SIMILARITY TO KYNURENI E 9.5 578 9 005159 PDHC (FRAGMENT).  6 9.5 478 3 Q18026 SIMILAR TO KYNURENI E 9.5 576 9 051939 TOLUGINE-3-MONODYGENAS COAD.  6 9.5 576 9 059463 SUBUNIT FOR LIGHT-INDE 6 9.5 576 9 050865 SOCD.  6 9.5 576 9 045664 SBSB GENE.  6 9.5 576 9 045664 SBSB GENE.  6 9.5 577 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 1             | 13    | 20.6    | 478    | 12 | 098995 |                        | 6.00e-1 |
| 6 9.5 146 9 050021 02266C.  9.5 214 3 018938 HYPOTHETICAL PROTEIN D 056836 ONF UL133.  6 9.5 275 1 066836 ORF UL133.  9.5 376 033292 CYTOCHROME B (FRAGMENT OFF) O34463 MALONIC COA-ACYL CARRI O55 317 9 005873 HYPOTHETICAL 34.9 KD P DHC (FRAGMENT).  6 9.5 366 9 006159 PDHC (FRAGMENT).  6 9.5 366 9 006159 SIMILARITY TO KYNURENI O55 31 005979 SIMILARITY TO THETICAL O55 31 005979 SIM | 2             | v     | σ       | 141    | ;  | C8090  |                        | 6 779+0 |
| 6 9.5 214 3 018938 HYPOTHETICAL PROTEIN D 6 9.5 257 11 068385 ORF UL133. 6 9.5 308 6 023292 DEHYDROGENAS. 6 9.5 308 6 025109 CYTOCHROME B (FRAGMENT D 7 9.5 317 9 034463 MALONYL COA-ACYL CARRI 6 9.5 366 9 006159 PHYPOTHETICAL 34.9 KD P 6 9.5 453 1 005979 SIMILARITY TO KYNURENI 6 9.5 478 3 026159 SIMILARITY TO KYNURENI 6 9.5 5019 9 051939 TOLUENE-3-MONOXYGENAS 6 9.5 506 9 055085 SOCD. 6 9.5 576 9 026193 COSCR 5 PROTEIN. 6 9.5 594 3 016312 CO5CR 5 PROTEIN. 6 9.5 524 9 016312 CO5CR 5 PROTEIN. 6 9.5 524 9 P72974 HYPOTHETICAL 68.9 KD P 6 9.5 526 8 643377 NITRAPE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | m             | œ     | 6       | 146    | ď  | 050021 |                        | 6 776+0 |
| 6 9.5 257 11 Q68385 ORF UL133. 6 9.5 370 9 033592 DEHYDROGENAGE. 6 9.5 317 9 034463 MALONYL COA-ACYL CARRI 6 9.5 317 9 034463 HYPOTHERICAL 34.9 KD P 6 9.5 453 10 005979 PDHC (FRAGMENT) 6 9.5 453 1 005979 SIMILARITY TO KYNURENI 6 9.5 508 9 P05463 SUBLIAR TO R. NORVEGIC 6 9.5 576 9 Q51939 TOLUGENE-3-MONODYGENAS 6 9.5 576 9 Q45664 SBSB GENE. 6 9.5 599 8 O22279 HYPOTHETICAL 68.9 KD P 6 9.5 590 9 Q45664 SBSB GENE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 4             | Φ.    | 5       | 214    | 'n | 018938 | PROTEIN                | 6.77e+0 |
| 6 9.5 272 9 033292 DEHYDROGENASE. 6 9.5 308 6 035109 CYTOCHROME B (FRAGMENT COA-ACIL CARRI COA-ACIL CARRI CAS. 230 9 005873 HYDOTHETICAL 34.9 KD P COS. 230 9 005873 HYDOTHETICAL 34.9 KD P COS. 230 9 005879 SIMILARITY TO KYRUNENI COA-ACIL CARRI CAS. 231 1005979 SIMILARITY TO KYRUNENI CAS. 250 9 0510305 SIMILARITY TO KYRUNENI CAS. 250 9 0510305 SUBUNIT FOR LIGHT-INDE COS. 250 9 165132 COS. 250 9 165132 COS. 250 9 165132 COS. 250 9 165132 HYPOTHETICAL GB.9 KD P COS. 250 9 165137 HYPOTHETICAL COS. 250 9 165664 SBSB GENE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ß             | ø     | 9       | 257    | H  | 068385 |                        | 6.77e+0 |
| 6 9.5 308 6 035109 CYTOCHROME B (FRAGMENT 6 9.5 317 9 034463 MALONIC COA-ACYL CARRI 6 9.5 366 9 005873 HYPOTHETICAL 34.9 KD P 05873 HYPOTHETICAL 34.9 KD P 05873 HYPOTHETICAL 34.9 KD P 05873 1 005979 SIMILARITY TO KYNURENI 6 9.5 501 9 051939 TOLUENE-3-MONOOXYGENAS 6 9.5 578 9 P95463 SUBUNIT FOR LIGHT-INDE 6 9.5 578 9 021312 CO5CB 5 PROTEIN. 6 9.5 594 3 016312 CO5CB 5 PROTEIN. 6 9.5 524 9 P72974 HYPOTHETICAL 68.9 KD P 6 9.5 524 9 P72974 SBSB GENE. 70.9 KD P 6 9.5 526 8 041377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 9             | 9     | 9.5     | 272    | σ  | 033292 | DEHYDROGENASE.         | 6.77e+0 |
| 6 9.5 317 9 034463 MALONYL COA-ACYL CARRI 6 9.5 330 9 005873 HYPOTHETICAL 34.9 KD P P P P P P P P P P P P P P P P P P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 7             | φ     | 9.5     | 308    | ø  | 035109 | CYTOCHROME B (FRAGMENT | 6.77e+0 |
| 6 9.5 330 9 005873 HYPOTHETICAL 34.9 KD P 6 9.5 366 9 006159 PDHC (FRAGMENT). 6 9.5 478 3 Q18026 SIMILARITY TO KYNURENI 6 9.5 501 9 Q51939 SIMILARITY TO KYNURENI 6 9.5 501 9 Q51939 TOLUGENE-3-MONOOXYGENAS 6 9.5 508 9 P95463 SUBUNIT FOR LIGHT-INDE 6 9.5 594 3 Q16312 CO5C8.5 PROTEIN. 6 9.5 599 8 CO2279 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 SBS GENE. 6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | æ             | 9     | 9.<br>S | 317    | σ  | 034463 | MALONYL COA-ACYL CARRI | 6.77e+0 |
| 6 9.5 366 9 006159 PDHC (FRAGMENT). 6 9.5 453 1 005979 SIMILARITY TO KYRURENI 6 9.5 501 9 021939 SIMILARITY TO REVRURENI 6 9.5 501 9 021939 TOLUENE-3-MONOOXYGENA 6 9.5 578 9 P95463 SUBUNIT FOR LIGHT-INDE 6 9.5 579 9 0250865 SOCD. 6 9.5 594 3 0.16312 CO5C8.5 PROTEIN. 6 9.5 599 8 022279 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 HYPOTHETICAL 68.9 KD P 6 9.5 926 8 045664 SBSB GENE. 6 9.5 926 8 043377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | σ             | 9     | 9.5     | 330    | σ  | 005873 |                        | 6.77e+0 |
| 6 9.5 453 1 Q05979 SIMILARITY TO KYNURENI 6 9.5 478 3 Q18026 SIMILARITY TO KNURENI 6 9.5 5019 9 Q51939 TOLUBRE-3-MONOXYGENA 6 9.5 508 9 P95463 SUBUNI FOR LIGHT-INDE 6 9.5 576 9 Q50865 SOCD. 6 9.5 594 3 Q16312 C05C8.5 PROTEIN. 6 9.5 599 8 Q22279 HYPOTHETICAL 68.9 KD P 6 9.5 524 9 P72974 HYPOTHETICAL 68.9 KD P 6 9.5 926 8 Q45664 SBSB GENE. 6 9.5 926 8 Q4377 NITRAPE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 10            | 9     | 9.5     | 366    | σ  | 006159 | PDHC (FRAGMENT).       | 6.77e+0 |
| 6 9.5 478 3 Q18026 SIMILAR TO R. NORVEGIC 6 9.5 501 9 Q21939 TOLUENB-3-MONOXYGENAS 6 9.5 576 9 Q50865 SOCD. 6 9.5 576 9 Q50865 SOCD. 6 9.5 594 3 O16312 C05C8.5 PROTEIN. 6 9.5 599 8 Q22279 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P 6 9.5 920 9 Q45664 SBSB GENE. 6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 11            | 9     | 9.5     | . 453  | Н  | 005979 | SIMILARITY TO KYNURENI | 6.77e+0 |
| 6 9.5 501 9 Q51939 TOLUGENE-3-MONOOXYGENAS<br>6 9.5 508 9 P99463 SUBUNIT FOR LIGHT-INDE<br>6 9.5 594 3 OL6312 CO5C8.5 PROTEIN.<br>6 9.5 599 8 O22279 HYPOTHETICAL 68.9 KD P<br>6 9.5 624 9 P72974 HYPOTHETICAL 68.9 KD P<br>6 9.5 926 9 Q45664 SBSB GENE.<br>6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 12            | 9     | 9.5     | 478    | m  | 018026 | SIMILAR TO R. NORVEGIC | 6.77e+0 |
| 6 9.5 508 9 P95463 SUBUNIT FOR LIGHT-INDE 6 9.5 576 9 050865 SOCD. 6 9.5 594 3 016312 C05C8.5 PROTEIN. 6 9.5 599 8 022279 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P 6 9.5 920 9 045664 SBSB GENE. 6 9.5 926 8 041377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 13            | 9     | 9.5     | 501    | σ  | 051939 | TOLUENE-3-MONOOXYGENAS | 6.77e+0 |
| 6 9.5 576 9 050865 SOCD.<br>6 9.5 594 3 016312 C05C8.5 PROTEIN.<br>6 9.5 599 8 022279 HYPOTHETICAL 68.9 KD P<br>6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P<br>6 9.5 920 9 045664 SBB GENE.<br>6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 14            | 9     | 9.5     | 508    | σ  | P95463 |                        |         |
| 6 9.5 594 3 016312 C05C8.5 PROTEIN.<br>6 9.5 599 8 022279 HYPOTHETICAL 68.9 KD P<br>6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P<br>6 9.5 920 9 045664 SBB GENE.<br>6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 15            | ø     | 9.5     | 576    | 0  | 050865 | SOCD.                  | 6.77e+0 |
| 6 9.5 599 8 022279 HYPOTHETICAL 68.9 KD P 6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P 6 9.5 920 9 Q45664 SBSB GENE. 6 9.5 926 8 QA1377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 16            | φ     | 9.5     | 594    | ო  | 016312 | C05C8.5 PROTEIN.       | 6.77e+0 |
| 6 9.5 624 9 P72974 HYPOTHETICAL 70.9 KD P 6 9.5 920 9 Q45664 SBSB GENE. 6 9.5 926 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 17            | φ     | 9.5     | 599    | ω  | 022279 | 68.9                   | 6.77e+0 |
| 9 Q45664 SBSB GENE.<br>8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 18            | Q     | 9.5     | 624    | 0  | P72974 | 70.9                   | 6.77e+0 |
| 8 Q41377 NITRATE REDUCTASE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 19            | φ     | 9.5     | 920    | σ  | 045664 | SBSB GENE.             | 6.77e+0 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 20            | φ     | 9.5     | 926    | 8  | 041377 | NITRATE REDUCTASE.     | 6.77e+0 |

HUMAN PAPILLOMAVIRUS TYPE 5. VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.

[1] SEQUENCE FROM N.A.

RAC OS RED DE DE LA COS RES CO

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M. 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                               |
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| FRUCTOSYLTRANSFERASE.  GRAVIN.  MASTHENIA GRAVIS AUTO GRAVIN.  MAGNESIUM CHELATASE SU 22 PREPRO-HALYSTATIN 3 (F 70 TO TRY SINOGEN (FRAGMENT)  14 ENVELOPE GLYCOPROTEIN 10 ENVELOPE GLYCOPROTEIN 10 ENVELOPE GLYCOPROTEIN 11 ENVELOPE GLYCOPROTEIN 12 ENVELOPE GLYCOPROTEIN 13 GP120 (FRAGMENT). 14 GRAVELOPE GLYCOPROTEIN 15 ENVELOPE GLYCOPROTEIN 16 GP120 (FRAGMENT). 17 GP120 (FRAGMENT). 18 GNVELOPE GLYCOPROTEIN 18 ENVELOPE GLYCOPROTEIN 19 ENVELOPE GLYCOPROTEIN 19 ENVELOPE GLYCOPROTEIN 19 ENVELOPE GLYCOPROTEIN 10 ENVELOPE GLYCOPROTEIN 11 ENVELOPE PROTEIN. 12 ENVELOPE PROTEIN. 13 PROTEIN A. 14 PROTEIN. 15 PROTEIN. 16 ENVELOPE PROTEIN. 17 ENVELOPE PROTEIN. 18 PROTEIN A. 18 PROTEIN. 19 PROTEIN. 19 PROTEIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 78 AA.  SATION UPDATE)  METAZOA; CHORDATA; SERPENTES; COLUBRO  R J.; 9-236(1996).  HELL ADHESION; VENO  14 CRC32; 14 CRC32; DB 12; Length 47 6.00e-15; Itches 2; Indels                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT; 141 AA.<br>CREATED)<br>LAST SEQUENCE UPDATE)<br>LAST ANNOTATION UPDATE)  |
| 9 055242<br>2 000310<br>2 000310<br>2 090970<br>10 00022<br>11 00022<br>11 011510<br>11 011510<br>11 0169971<br>11 069971<br>11 069971<br>11 073363<br>11 036355<br>11 036355<br>11 036355<br>11 036355<br>11 036355<br>11 036355<br>11 036355<br>11 036355                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNME  INARY; PRT;  O2, CREATE  O5, LAST A  ILEVANTINE VI  ILEVANTINE VI  SCLEROGLOS  MACROVIPERA.  ' TU A.T., S  COMMUN. 224  ' TU B.T., S  COMMUN. 224  ' TU B.T., S  COMMUN. 224  ' TU A.T., S  COMUN. 224  ' TU A.T., S  COMMUN. 224  ' TU A.T., S  COMUN. 224  ' TU A.T., S  COMMUN. 224  ' TU A.T., S  COMMUN. 224  '                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                               |
| 99.55<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684<br>10.684 | 1 1110 01                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | FLRAGTVCKRAVGDD 459                                                           |
| <b>֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍֍</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 9895;<br>1-FEB-1997<br>1-FEB-1997<br>1-JAN-1998<br>EBETASE LE:<br>ACROVIDERA<br>ACROVIDERA<br>ACROVIDERA<br>IL PERIDAE;<br>IL PERIDAE;<br>IL PERIDAE;<br>IL SUB-VENO<br>IL SUB | 31<br>31<br>8092<br>8092<br>8092<br>11-NO<br>11-NO<br>11-NO<br>11-NO<br>11-NO |
| 00000000000000000044444444000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT 1D 0989 AC 0989 AC 0989 DT 01-5 DT 01-6 DT 01-6 DE LEBE OC EURA OC VIPE RP SEQUENT RP SEQUENT RP SEGUENT RP SEGUEN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | DD OY NE SULT                                                                 |

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05,
05,
05,
 PRELIMINARY;
 9.5%;
Local Similarity 100.0%;
Les 6; Conservative
 MIVUUZ.15.
MYCOBACTERIUM TUBERCULOSIS.
 017 6 PRELIMINAR 03329; 01-3AN-1998 (TREMBLREL. 0 01-3AN-1998 (TREMBLREL. 0 01-3AN-1998 (TREMBLREL. 0 DEHYDROGENASE.
 STRAIN=TOLEDO;
MEDLINE; 96099416.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 154 AVGDDV 159
 97 CISGPC 102
 41 AVGDDV 46
 20 CISGPC 25
 STRAIN-H37RV;
 STRAIN-H37RV;
 STRAIN-H37RV
 Query Match
 Matches
 RESULT
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 ID ACCOOR SERVING THE REPORT OF THE REPORT O
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 Gaps
 Gaps
 CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
 MEDLINE; 94150718.
MEDLINE; 94150718.
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., FULTON L., JONES M., KERSHAW J., KIRSTEN J., LASTSTER N., LATRELLLE P., LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
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 ö
 MYCOBACTERIUM LEPRAE.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
 Score 6; DB 11; Length 141;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 Score 6; DB 9; Length 146;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 SEQUENCE FROM N.A.
FARMER A.D.;
FARMER A.D.;
ENGLIST (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENGL; U31790; G1020259; -.
SEQUENCE 141 AA; 16410 MW; 191F191F CRC32;
DELIUS H.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 ROBISON K.;
SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 015182; G699215; -.
SEQUENCE 146 AA; 15516 MW; 2530B171 CRC32;
 SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN D1053.1.
 214 AA.
 SEQUENCE FROM N.A.
MEDLINE; 90012349.
FAVRE M., OBALEK S., JABLONSKA S., ORTH G.;
J. VIROL. 63:4910-4910(1989).
 146 AA
 PRT;
 PRT;
 PRELIMINARY;
 01,
01,
 PRELIMINARY;
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
 SEQUENCE FROM N.A. SMITH D.R.;
 SEQUENCE FROM N.A.
 132 CCRNCY 137
 30
 17 AVGDDV 22
 111111
41 AVGDDV 46
 111111
25 CCRNCY
 LT 4
018938
018938;
 050021;
 LT 3
Q50021
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CHA T.A., TOM E., KEMBLE G.W., DUKE G.M., MOCARSKI E.S., SPAETE R.R.;
J. VIKOL. 70:78-83141996).
EMBL: U33331; G1167918; — SEQUENCE 257 AA; 27471 MW; EC259DCB CRC32;
 Gaps
 Gaps
 ORF UL133.
HUMAN CYTOMEGALOVIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
 MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
CROE S.T.;
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; ALO08967; E1173880; -.
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STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATENON A., WEINSTOCK L., WALKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).
EMBL. 26560, E349049.
EMBL. 26560, E349049.
SEQUENCE 214 AA; 23656 MM; 84DA48C3 CRC32;
 PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
 Score 6; DB 11; Length 257;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 Query Match 9.5%; Score 6; DB 3; Length 214; Best Local Similarity 100.0%; Pred. No. 6.77e+00; Matches 6; Conservative 0; Mismatches 0; Indels
 MURPHY L., HARRIS D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
 PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
 Q68385 PRELIMINARY; PRT; 257 AA. Q68385 Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-NOV-1996 (TREMBLREL. 01, LAST SANNOTATION UPDATE)
 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 CREATED)
 PRT;
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| 51 SGITPD 56
 80 SGITPD 85
 STRAIN-H37RV
 MTCY20B11.03
 STRAIN-H37RV
 STRAIN-168;
 COLE S.T.;
 005873
 RESULT
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 C STRAIN-168;

AZEVEDO V. BERTEREO M.C., BESSIERES P., BOLOTIN A., BOCHERY S.,
AZEVEDO V., BERTERO M.C., BESSIERES P., BOLOTIN A., BOCHERY S.,
BORRISS R., BOURSIER L., BRAUN M., BRIGNELL S.C., BRON S.,
BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
A BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
A BROUILLET S., BRUSCHI C.V., CONDERTON I.F., COMMINGS N.J., EMBREIG R.A.,
A BRIADOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMBREIGON P.T.,
A BRIADAN K.D., ERRINGTON J., FERRARI E., FOULGER D.,
A GUISEPE C., FUJITA Y., FUMA S., GALIZZI A., GRALERON N.,
AGINESPE G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENDUT A.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
AORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
 LEETON P.R., CHRISTIDIS L., WESTERMAN M., BOLES W.E.;
AUK 111:831-841(1994).
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
FERROCYTOCHROME C.
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
 BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 EUKARYOTA; ANIMALIA; META2OA; CHORDATA; VERTEBRATA; AVES; NEORNITHES;
NEOGNATHAE; PSITTACIFORMES.
 EMBL; U13623; G535329; -- PROSITE; PS00192; CYTOCHROME_B_HEME; 1. MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;
 Gaps
 Gaps
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 ö
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39).
FABD OR YLPE.
 Score 6; DB 6; Length 308; Pred. No. 6.77e+00; 0; Mismatches 0; Indels
 DB 9; Length 272;
6.77e+00;
atches 0; Indels
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 1 1
308 308
308 AA; 34149 MW; 15EC3616 CRC32;
28223 MW; 11FBA0FD CRC32;
 Score 6; DB 9;
Pred. No. 6,77e+
0; Mismatches
 317 AA.
 308 AA
 PRT;
 PRT;
 O1-NOV-1996 (TREMBLREL. 01, C
01-NOV-1996 (TREMBLREL. 01, L.
01-JAN-1998 (TREMBLREL. 05, LL
CYTOCHROME B (FRAGMENT).
MELOPSITTACUS UNDULATUS.
MITOCHODRION.
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 035109 PRELIMINA
035109;
01-NOV-1996 (TREMBLREL.
 ¥.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 196 NSVHPC 201
 178 GITPDC 183
 111111
52 GITPDC 57
 1 NSVHPC 6
 LISSUE-LIVER;
 NON_TER
NON_TER
SEQUENCE
SEQUENCE
 O34463
O34463;
 RESULT
 RESULT
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KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,

KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,

LEE S.M., LEVINE A., LIU H., MASUDA S., MADEL C., MEDIGUE C.,

MEDIAN N., MELLADO R. D., OGTWARA S., NAREL S., NEDIGUE C.,

NOONE D., O'REILLY M., OGTWARA A., OUDEGA B., PARK S.H.,

PARRO V., POHL T.M., PORTETELLE D., PORMULIK S., PRESCOTI A.M.,

REGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,

RAIGER M., RIVOLTA C., SCHLEICH S., SCHOPORT G., REY M., REYNOLDS S.,

RAIGHT S., SCANLAN E., SCHLEICH S., SCHOPORT F., SCAPAIE Y.,

A SCHOULI J., SEKOWAR A., SEROR S.J., SERROR P., SOFONE F.,

A SOROKIN A., TAMAROSHI A., TAKAHASHI H., TAKERARU K.,

TAKEUCHI M., TAMAROSHI A., TANARA T., TERPETRA P., TOGNONI A.,

TOSATO V., UCHITMAM S., VANDENBOL M., VANNIER F., VASSAROTTI A.,

MINTERS P., WIPPA TA., YAMAMOTO H., YANANE K., YASSAROTTI A.,

MINTERS P., WIPPA TA., YAMAMOTO H., YANANE K., YASSUMOTO K., YATA K.,

NOSHIRAMA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;

LU NATURE 390:249-256(1997).
 m,
 Gaps
 MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 ö
 PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
 Score 6; DB 9; Length 317;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 0; Indels
 SEVELLE.
STRAIN-168;
FOULGER D., ERRINGTON J.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299112; E11851891; -.
EMBL; Y13937; E323514; -.
TRANSFERASE; ACYLTRANSFERASE.
SEOUENCE 317 AA; 34035 MW; 3F1322C4 CRC32;
 STRAIN=H37RV;
BADCOCK K., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 04, CREATED)
04, LAST SEQUENCE UPDATE)
04, LAST ANNOTATION UPDATE)
 PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL: 295121; E314514; -
HYPOTHETICAL PROTEIN.
SEQUENCE 330 AA; 34875 MW: CRC57ARF CDC20.
 330 AA
 PRT;
 01-JUL-1997 (TREMBLREL. 04, CI
01-JUL-1997 (TREMBLREL. 04, LA
01-JUL-1997 (TREMBLREL. 04, LA
HYPOTHETICAL 34.9 KD PROTEIN.
 PRELIMINARY;
 Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
 MYCOBACTERIUM TUBERCULOSIS.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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WATERSTON R.; SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 EMBL; U19027; G609377; -. SEQUENCE 453 AA; 51032 MW; F015FAB2 CRC32;
 PRELIMINARY;
 / Match .9.5%;
Local Similarity 100.0%;
nes 6; Conservative
 9.5%;
Local Similarity 100.0%;
hes 6; Conservative
 C15H9.7.
CAENORHABDITIS ELEGANS
 [3]
SEQUENCE FROM N.A.
STRAIN-S28BC (AB972);
 STRAIN-S288C (AB972);
 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2; BENTLEY D.;
 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
 166 EPREGE 171
 204 EPREGE 209
 13 EPREGE 18
 ||||||
|13 EPREGE 18
 HALLSWORTH K.;
 Query Match
 Query Match
 RESULT 12
10 018026
10 018026
10 01-NOV-1

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Matches
 Matches
 RESULT
ID Q5
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 Gaps
 Gaps
 MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 SEQUENCE FROM N.A.
STRAIN-$288C (AB972);
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
TAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,
KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
JOHNSTON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T.,
MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUSO D.,
RIFKEN L., RILES L., TARICH A., TREVASKIS E., VICHATI D.,
WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
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 PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
 0; Indels
 Score 6; DB 9; Length 366;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 Score 6; DB 9; Length 330;
Pred. No. 6.77e+00;
 GATTUNG S., DEVLIN K., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
 BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL: 295556; E316908; -.
NON_TER 366 366
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
 NON_TER 366 366
SEQUENCE 366 AA; 38071 MW; A9B7D541 CRC32;
 0; Mismatches
 366 AA
 453 AA
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ)
01-NOV-1996 (TREMBLREL. 01, LAST ANN
 PRT;
 PRT;
 01-JUL-1997 (TREMBLREL. 04, 01-JUL-1997 (TREMBLREL. 04, 01-JUL-1997 (TREMBLREL. 04,
 PRELIMINARY;
 PRELIMINARY;
Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match 9.5%;
Best Local Similarity 100.0%;
 MYCOBACTERIUM TUBERCULOSIS
 SIMILARITY TO KYNURENINASE
 6; Conservative
 SEQUENCE FROM N.A. STRAIN-H37RV;
 [2]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 (FRAGMENT)
 30 AVGDDV 35
 72 VGDDVD 77
 111111
42 VGDDVD 47
 41 AVGDDV 46
 STRAIN-H37RV;
 STRAIN-H37RV;
 COLE S.T.;
 LT 10
006159
006159;
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005979
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 Gaps
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 EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 MILSON R., ALINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J.,
COULSON A., CRAXTON M., DEAR S., DU Z., DIRBIN R., FAVELLO A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
JATREBLLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTHORE B.,
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPEA A.,
SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
VAUGHAN K., WATERSTON J., THIERRY-MIEG J., THOWAS K., VAUDIN M.,
WILKINSON-SPROAT J., MOHLDMAN P.;
NITKINSON-SPROAT J., WOHLDMAN P.;
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DB 1; Length 453;
6.77e+00;
atches 0; Indels
 0; Indels
 Score 6; DB 3; Length 478; Pred. No. 6.77e+00;
 SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U56965; G1293837; -.
SEQUENCE 478 AA; 54049 MW; 274B0462 CRC32;
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 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) SIMILAR TO R. NORVEGICUS KYNURENINASE.
 LT 13
051939
051939
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01-00V-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Score 6; DB 1;
Pred. No. 6.77e+
0; Mismatches
 478 AA
 0; Mismatches
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1996 (TREMBLREL. 01, LAST ANN
 PRT;
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Search completed: Fri Sep 25 13:21:10 1998 Job time : 14 secs.
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51 SGITPD 56
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 P95463
P95463;
01-mar-1997 (TREMBLREL. 03, CREATED)
01-mar-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SUBUNIT FOR LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE.
 Score 6; DB 9; Length 501;
Pred. No. 6.77e+00;
0; Mismatches 0; Indels
 2; Indels
 Score 6; DB 9; Length 508;
Pred. No. 6.77e+00;
0; Mismatches 2; Indels
 MIXOCOCCUS XANTHUS.
PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; MIXOBACTERALES;
MIXOCOCCACEAE.
 9.5%; Score 6; DB 9; Length 576;
 PSEUDOMONAS PICKETTII.
PROKARYOTA; BACTERIA; GRACILICUTES; SCOTOBACTERIA;
AEROBIC RODS AND COCCI; PSEUDOMONADACEAE; PSEUDOMONAS.
 01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) TOLUENE-3-MONOOXYGENASE OXYGENASE SUBUNIT.
 STRAIN-IAM-MIO1;
FUJITA Y., TAKAGI H., HASE T.;
PLANT CELL PHYSIOL. 37:313-323(1996).
EMBL: D7808; D1011974;
SEQUENCE 508 AA; 56819 MW; B752937C CRC32;
 BYRNE A.M., KUKON J.J., OLSEN R.H.;
GENE 154:65-70(1995).
EMBL: U04052; G505046; -.
SMOOXYGENASE.
SEQUENCE 501 AA; 57555 MW; BA29CF85 CRC32;
 PLECTONEMA BORYANUM.
PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
 576 AA.
 PRT;
 PRELIMINARY;
 Duery Match
Best Local Similarity 100.0%;
Matches 6; Conservative
 Ouery Match
Best Local Similarity 75.0%;
Matches 6; Conservative
 115 050865 PRELIMINAR 050865 050865, 01-NOV-1996 (TREMBLREL. 0 01-NOV-1999 (TREMBLREL. 0 01-JAN-1998 (TREMBLREL. 0
 STRAIN-PKO1;
MEDLINE; 95172404.
 SEQUENCE FROM N.A.
STRAIN-LS500;
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 328 LLAGIYCK 335
 32 LXAGTXCK 39
 349 GITPDC 354
 111111
52 GITPDC 57
 Query Match
 CHLB.
 RESULT

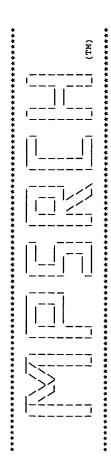
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Gaps
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Best Local Similarity 100.0%; Pred. No. 6.77e+00; Matches 6; Conservative 0; Mismatches 0; Indels
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protein . protein database search, using Smith-Waterman algorithm srch\_pp

MasPar time 4.28 Seconds 253.467 Million cell updates/sec Fri Sep 25 13:17:51 1998; Run on:

not generated Tabular output >PCT-US98-16719-19 (1-67) from PCTUS9816719A.pep 506 Description: Perfect Score:

1 NSVHPCCDPVKCEPREGEHC.....DYCSGITPDCPRNRYKXKXD Sequence:

67

PAM 150 Gap 11 Scoring table:

131922 seqs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq32
l:part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 22.part22 23.part23
24.part24 25.part25 26.part26 27.part27 28.part28
29.part29

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 24.774; Variance 96.234; scale 0.257

tatistics:

|                 | Query     | ,      |                       |          |
|-----------------|-----------|--------|-----------------------|----------|
| Match Length DB | ngth DB I | Ω      | Description           | Pred. No |
| 56.3            | 73 23 WJ  | W14083 | Platelet aggregation  | 9.05e-20 |
| 55.7            | ~         | 306494 | Platelet aggregation  | 1.85e-1  |
| 53.6            | 480 8 R4  | R42867 | Platelet aggregation  | 2.55e-1  |
| 52.6            | 10        | R53942 | Disintegrin peptide # | 8.36e-18 |
| 52.6            | 72 3 R.   | R10109 | Trigramin-beta 1      | 8.36e-18 |
| 52.6            | 73 3 R.   | R10110 | Trigramin-beta 2.     | 8.36e-18 |
| 52.4            | 97 5 R.   | R28705 | Bifunctional inhibito | 1.06e-1  |
|                 | 7 5       | R28708 | Bifunctional inhibito | 1.06e-1  |
|                 | 20        | R25150 | Bifunctional inhibito | 1.06e-17 |
| 52.4            |           | R25154 | Bifunctional inhibito | 1.06e-1  |
|                 | ហ         | R28707 | Bifunctional inhibito | 2.74e-1  |
| 51.6            | 'n        | R28703 | Bifunctional inhibito | 2.74e-1  |
|                 | 'n        | R28704 | Bifunctional inhibito | 2.74e-17 |
| 51.6            | . 5       | R28706 | Bifunctional inhibito | 2.74e-1  |
| 51.6            | 0         | R25149 | Bifunctional inhibito | 2.74e-17 |
| 51.6            | 'n        | R25153 | Bifunctional inhibito | 2.74e-17 |
| 51.6            | 106 5 R   | R25152 | Bifunctional inhibito | 2.74e-17 |
| 51.6 1          |           | 0      |                       |          |

| 5.57e-17<br>7.05e-17<br>7.05e-17<br>7.05e-17<br>7.05e-17<br>7.05e-17<br>7.05e-17<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e-15<br>1.20e- |
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| Albolabrin peptide ta Albolabrin. Trigramin-gamma. Disintegrin peptide # Bifunctional inhibito Bifunctional inhibito Bifunctional inhibito Bifunctional inhibito Bifunctional inhibito Bishtegrin peptide # Batroxostatin. Echistatin-alpha 2. Sequence of viper ven Nid type disintegrin platelet adhesion blo Platelet adhesion blo Disintegrin peptide # Example of cysteiner ven Sequence of viper ven Echistatin with Asp o Disintegrin peptide # Sequence of viper ven Elegantin peptide tar Blatelet adhesion blo Sequence of viper ven Platelet adhesion blo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| W45500<br>R06395<br>R53946<br>R25147<br>R25147<br>R25147<br>R25147<br>R25147<br>R25147<br>R25147<br>R25147<br>R2428<br>P911098<br>P911098<br>P911098<br>P911098<br>P911099<br>R34291<br>R34291<br>R53937<br>R24289<br>R34299<br>R34289<br>R34289<br>R34289<br>R34289                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 28<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| CCCC0000CC44444444444446666666666666666                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 0.000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 110<br>2210<br>2210<br>2210<br>2210<br>2310<br>2310<br>24444<br>2510<br>2610<br>2610<br>2610<br>2610<br>2610<br>2610<br>2610<br>26                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

### ALIGNMENTS

```
Doo SK, Hak DK, Hong MM, In CK, Jeong HY, Kwang HC;
Soo JL, Yung DY,
WPI: 97-121376/12.
Peptide derived from Korean salmosa viper venom - useful as blood
patcalet aggregation inhibitor, for the management of thrombosis
Claim 1; Page 11: 15pp; French.
This peptide, designated Salmosin, inhibits blood platelet aggregation.
It is derived from the venom of the Korean salmosa viper (Agkistrodon halys brevicaudus). Salmosin can be used, in particular, in compositions for management of thrombosis. Salmosin also has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections of the Korean salmos has higher activity than sections.
 27-0cT-1997 (first entry)
Platelet aggregation inhibitor, Salmosin.
Salmosin; Inhibit; blood; platelet aggregation; venom; Korean;
salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.
PR2736266-Al.
 Gaps
 Score 285; DB 23; Length 73;
Pred. No. 9.05e-20;
11; Mismatches 17; Indels 0;
 10-JAN-1997.
24-AUG-1995; O10049.
26-JUL-1995; KR-019685.
(MGGA-) MOGAM BIOTECHNOLOGY RES INST.
(WAKI-) ZH MARIWA SEIMEI KOGAKU KENKYUSHO.
DOO SK, Hak DK, Hong MM, In CK, Jeong HY, Kwang HC;
 R06494 standard; protein; 73 AA.
R06494;
04-JAN-1991 (first entry)
Platelet aggregation inhibitor.
Snake venom; thromboxan A2; thrombosis; anti-coagulant.
 standard; peptide; 73 AA
 Query Match 56.3%;
Best Local Similarity 52.5%;
Matches 31; Conservative
 73 AA;
 Sequence
 LT 1
W14083 s
 W14083;
 RESULT
ID RO
AC RO
DT 04
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RESULT
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Claim 24, Page 46; 62pp; English.

The sequences given in R3393-46 are disintegrin peptides.

Disintegrins are low molecular weight proteins from the Viperidae family of snakes which bind integrin proteins similar to the endogenous messenger and structurally interactive molecules.

Disintegrins are competitive inhibitors of biomolecules, such as fibrinogen, for integrin binding sites such as GP IIb/IIIa on human platelets. Disintegrins contain the tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides, can be used for the treatment and
 Disintegrin peptide #10.
Disintegrin; Viperidee; snake; integrin; inhibitor; fibrinogen; integrin binding sites; GP IIb/IIIa; human; platelets; radiolabel; treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli; tumours; abscesses; thrombus component.
 arterial thrombi, pulmonary emboli and tumours or abscesses having a thrombus component.
 Radio-labelled polypeptide(s) derived from Viperidae
 diagnosis of venous and arterial thrombi, tumours or abscesses that have a thrombus
 Query Match
Best Local Similarity 52.5%;
Matches 31; Conservative
 (first entry)
 05-0CT-1994.
05-0CT-1992; U09523.
19-0CT-1992; US-965674.
(UTEM) UNIV TEMPLE.
Knight LC, Maurer AH;
WPI; 94-151248/18.
 Agkistrodon piscivorous
 disintegrin(s) -
 21-DEC-1994
 IIA-GP IIIA.
 WO9409036-A
 Sequence
 Sequence
 R10109;
 Matches
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 rused for preventing agglutination and release in vivo or vitro,
and new recombinant DNA encoding it.
and new recombinant DNA encoding it.
Claim 3; Fig 9; 73pp; English.
The sequence is deduced from the coding strand of a synthetic
gene for a polypeptide inhibitor of platelet activation. The
polypeptide is analogous to that obtd. from the venom of
Agkistrodon p. piscivorus (North American Water Moccasin). The
gene can be used to produce recombinant inhibitor or fusion
proteins with eq. hirudin derivs. These can be used to decrease/
inhibit platelet aggregation and release in vivo or in vitro.
Usual dose is 0.01-100 mg/Kg body wt. The recombinant protein can
also be used to coat the surfaces of invasive medical devices.
 Gaps
 Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example; Page 33-35; 50pp; Japanese. The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
 Gaps
 It can also block stenosis and spasm at the site of thrombosis (by inhibiting the release of thromboxan A2).
See also R06508.
 ö
 ö
 Platelet aggregation inhibitory peptide.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
 Length 480;
 Score 282; DB 2; Length 73;
Pred. No. 1.85e-19;
10; Mismatches 18; Indels
 Score 271; DB 8; Length 480
Pred. No. 2.55e-18;
11; Mismatches 18; Indels
 (BIOG-) BIOGEN INC.
(UYBO-) BOSTON UNIV.
Maraganore JM, Jakubowski JA, Chao BH; WPI; 90-260891/34.
N-PSDB; Q05730.
 T
R42867 standard; Protein; 480 AA.
 03-OCT-1991; 256234.
26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 93-346841/44.
N-PSDB; Q50394.
 Query Match 53.6%;
Best Local Similarity 50.8%;
Matches 30; Conservative
 Query Match 55.7%;
Best Local Similarity 52.5%;
Matches 31; Conservative
 11-MAY-1994 (first entry)
 27-JAN-1989; US-303590.
 27-JAN-1989; US-303585.
01-NOV-1989; US-430313.
 26-JAN-1990; U00465
 Sequence 480 AA;
 09-AUG-1990
 05-0CT-1993
 Sequence
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Score 266; DB 10; Length 71; Pred. No. 8.36e-18; 9; Mismatches 18; Indels

pulmonary emboli and

for treatment and diagnosis of venous and

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 0; Gaps
13 npccdaatcklrpgaqcaqglccdqckfmkegtvc-rargddvndycngisagcprnpf 70
 Disclosure; Fig 11; 91pp; English.

The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.

See also R10106-R10113
 10 spanpccdaatckllpgaqcgegpccdqcsfmkkgticrrargddlddycngrsagcprn
 Platelet aggregation inhibitor; snake venom; fibrin binding;
 Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to
 Length 72;
 12; Mismatches 20; Indels
 Score 266; DB 3;
Pred. No. 8.36e-18;
 inhibition; GP IIA; GP IIIA; hypercoagulation. Trimesurius gramineus. W09015072-A.
 .r 5
R10109 standard; Protein; 72 AA.
 th 52.6%; Similarity 48.4%; 30; Conservative
 13-MAR-1991 (first entry)
 13-DEC-1990,
07-JUN-1990; U03216.
07-JUN-1989; US-362718.
(GETH) GENENTECH INC.
 Lazarus RA, Dennis MS;
WPI; 91-007159/01.
 Query Match
Best Local Similarity
 Trigramin-beta
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RESULT 4 ID R53942 standard; peptide; 71 AA.

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R25150;
04-JAN-1993
 Synthetic.
WO9210575-A.
 04-JAN-1993
 Synthetic.
WO9210575-A.
 25-JUN-1992
 Sequence
 Query Match
 Matches
 8888888
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 Bi: functional inhibitors of thrombin and platelet activation - comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions
Claim 5; Page 24; 103pp; English.
This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as N-appilog(Leu65). The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #7.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 spanpccdaatckllpgaqcgegpccdqcsfmkkgticrrargddlddycngrsagcprn 69
 :::||||: | :| ||:| || || || || ||:| ||:| ||:| ||:| ||:| ||:| ||: ||| ||: ||: ||:| ||: ||:| ||: ||: ||:| ||: ||: ||:| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
 Gaps
 Disclosure, Fig 11, 91pp, English.
The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.
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 Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition; GP IIA; GP IIIA; hypercoagulation. Trimesurius gramineus. W09015072-A.
 Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to
 Score 266; DB 3; Length 73;
Pred. No. 8.36e-18;
12; Mismatches 20; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
 R28705 standard; Protein; 97 AA.
 R10110 standard; Protein; 73 AA
 52.68;
 (first entry)
 Conservative
 05-DEC-1991; U09108.
07-DEC-1990; US-623611.
(BIOJ) BIOGEN INC.
 07-JUN-1989; US-362718.
(GETH) GENENTECH INC.
Lazarus RA, Dennis MS;
WPI; 91-007159/01.
 See also R10106-R10113
 13-DEC-1990.
07-JUN-1990; U03216.
 Best Local Similarity
Matches 30; Conserv
 rrigramin-beta 2
 13-MAR-1991
 IIA-GP IIIA
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Claim 7; Page 25; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet

activation and thrombin, and is referred to as C-appilog(leu4).

The inhibitor also contains a thrombin inhibiting component. The

inhibitor is used to inhibit thrombin and platelet-mediated processes

in patients or in extracorporael blood. It inhibits clot formation

and growth caused by platelets and clot accretion caused by fibrin

deposition, but do not cause thrombocytopaenia. The usual dose is

tlug-5mg/Kg/day opt. combined with a thrombolytic agent such as

tissue plasminogen activator. The inhibitor may be used to treat

or prevent myocardial infarction, or thrombosis; increase reocclusion

time; decreasing repertusion time; and inhibiting metastatic cell

growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 ö
 ö
lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80. Sequence 97 AA;
 Bifunctional inhibitor of platelet activation and thrombin #14.

bifunctional inhibitor; platelet activation; thrombin; inhibit clot;
formation; accretion; fibrin deposition; myocardial infarction;
thrombosis; increasing reocclusion time; decreasing reperfusion;
time; inhibiting metastatic cell growth.
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #6.
bifunctional inhibitor; platelet activation; thrombin; inhibit clot;
formation; accretion; fibrin deposition; myocardial infarction;
thrombosis; increasing resocclusion time; decreasing reperfusion;
time; inhibiting metastatic cell growth.
 Gaps
 0; Gaps
 38 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpf 96
 ## #PCCDPVKCEPREGEHCISGPCCRNCYFLXAGTXCKRAVGDDVDDYCSGITPDCPRNRY 62
 14 npcddaatcklrpgagcaeglccdqckflkegtvcrrargddvndycngisagcprnpf 72
 ö
 WPI; 92-234630/28.
Bi:functional inhibitors of thrombin and platelet activation comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombolic diseases, atherosclerosis,
 Score 265; DB 5; Length 97; Pred. No. 1.06e-17; 9; Mismatches 19; Indels
 Score 265; DB 5; Length 97;
Pred. No. 1.06e-17;
9; Mismatches 19; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS;
 Š
 R28708 standard; Protein; 97 AA.
 98
 / Match 52.4%; Local Similarity 52.5%; nes 31; Conservative
 Ouery Match
Best Local Similarity 52.5%;
Matches 31; Conservative
 R25150 standard; Protein;
 05-DEC-1991; U09108.
07-DEC-1990; US-623611.
(BIOJ) BIOGEN INC.
 97 AA;
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15 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpf
 T 11
R28707 standard; Protein;
 07-DEC-1990; US-623611.
 05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 05-DEC-1991; U09108
 Local Similarity
 (BIOJ) BIOGEN INC.
 30;
 Synthetic.
WO9210575-A.
 WO9210575-A.
 25-JUN-1992
 Synthetic
 Query Match
 R28703;
 R28707
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 Matches
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 cancer and neuro:degenerative conditions.

Claim 5: Page 23: 103pp: English.

This sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as Ile-Met-Nappilog(Leu65).

The inhibitor also contains a thrombin inhibiting component. The inhibitor also contains a thrombin and platelet-mediated processes in patients or in extraoorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin and growth caused by platelets and clot accretion caused by fibrin and growth combined with a thrombolytic agent such as lug-5mg/Kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 Comprise glyco:protein IIB or IIIa and thrombin inhibitory
moleties, for treating thrombotic diseases, atherosclerosis,
cancer and neuro:degenerative conditions

This sequence represents the bifunctional inhibitor of platelet
This sequence represents the bifunctional inhibitor of platelet
The inhibitor also contains a thrombin inhibiting component. The
Inhibitor is used to inhibit thrombin and platelet-mediated processes
in patients or in extracorporeal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombocytopaenia. The usual dose is
tissue plasminogen activator. The inhibitor may be used to treat
cor prevent myocardial infarction, or thrombosis; increase reocclusion
 ö
 04-JAN'1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #13.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 Gaps
 39 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpf 97
 decreasing reperfusion time; and inhibiting metastatic cell 1. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80 nce 98 AA;
 ö
 activation
 Bi:functional inhibitors of thrombin and platelet activation comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis,
 Score 265; DB 5; Length 98;
Pred. No. 1.06e-17;
 Score 265; DB 5; Length 98;
Pred. No. 1.06e-17;
9; Mismatches 19; Indels
 9; Mismatches 19; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
 Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
 R25154 standard; Protein; 98 AA. R25154;
 52.4%;
 52.4%;
52.5%;
 Best Local Similarity 52.5%;
Matches 31; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
(BIOJ) BIOGEN INC.
 US-623611.
 Query Match
Best Local Similarity
 07-DEC-1990; US-62:
(BIOJ) BIOGEN INC
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31; Conservative

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cancer and neuro-idegenerative conditions and recognizing the conditions of the cancer and neuro-idegenerative conditions.

Claim 7: Page 24: 103pp: English.

This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as Met-C-appilog. The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin
 reocclusion
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #11.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 04-JAN'1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #3.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fiprin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 62
73
 Gaps
 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpf 71
 time; decreasing reperfusion time; and inhibiting metastatic cell
growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
Sequence 96 AA;
 deposition, but do not cause thrombocytopaenia. The usual dose is ing-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclus
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions Claim 5; Page 23; 103pp; English.
This sequence represents the bifunctional inhibitor of platelet
 ö
 Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
Bi:functional inhibitors of thrombin and platelet activation
 Bi:functional inhibitors of thrombin and platelet activation
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombotic diseases, atherosclerosis,
 Length 96;
 19; Indels
 (BIOJ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
 Score 261; DB 5; I
Pred. No. 2.74e-17;
10; Mismatches 19;
 96 AA.
 R28703 standard; Protein; 96 AA.
 51.6%;
llarity 50.8%;
Conservative
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PI Eliforctional inhibitors of thrombin and platelet activation - comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions cancer and neuro:degenerative conditions cancer and neuro:degenerative conditions.

Claim 5; Page 23; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as Met-Nappling. The activation and thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibiting component. The inhibitor are or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat the decreasing reperfusion time; and inhibiting metastatic cells growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
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 The inhibitor
activation and thrombin, and is referred to as N-appilog. The inhibito also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #4.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #10.
bifunctional inhibitor; platelet activation; thrombin; inhibit clot;
 Gaps
 0; Gaps
 npcddaatcklrpgagcaeglccdgckfmkegtvcrrargddvndycng1sagcprnpf 95
 ő
 Score 261; DB 5; Length 97;
Pred. No. 2.74e-17;
10; Mismatches 19; Indels
 Length 96;
 10; Mismatches 19; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS;
 Score 261; DB 5;
Pred. No. 2.74e-17;
 J. 13
R28704 standard; Protein; 97 AA.
 T 14
R28706 standard; Protein; 97 AA.
R28706;
 51.6%;
llarity 50.8%;
Conservative
 Similarity 50.8%;
30; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 Best Local Similarity
Matches 30; Conserv
 (BIOJ) BIOGEN INC.
 Query Match
Best Local Similarity
Matches 30; Conserv
 92-234630/28
 97 AA;
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 Query Match
 R28704;
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cancer and neuro-degenerative conditions.

Claim 7; Page 24; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet

activation and thrombin, and is referred to as C-appilog.

The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is 1ug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat to prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 Cancer and neuroidegenerative conditions
Calaim 5: Page 23: 103pp: English.

Claim 5: Page 23: 103pp: English.

This sequence represents the bifunctional inhibitor of platelet
activation and thromble, and is referred to as Ala-Asn-Ser-N-appilog.

The inhibitor also contains a thromble inhibiting component. The
inhibitor is used to inhibit thromble inhibitish clot formation
in patients or in extracorporeal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombosytopaenia. The usual dose is
tissue plasminogen activator. The inhibitor may be used to treat
or prevent myocardial infarction, or thrombolytic gents such as
the decreasing reperfusion time; and inhibiting metastatic cell
growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #5.
bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
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 | WOSLING. | WOSLING. | WOSLING. | WOSLING. | WOSLING. | WOSLING. | WOSTING. | WOSTING. | WAS A BLOJ | BIOGEN INC. | WAS A BLOJ | BIOGEN INC. | WPI: 92-234630/28. | WPI: 92-234630/28. | WPI: 92-234630/28. | WI comprise glyco:protein IIB or IIIa and thrombin inhibitory | Toomprise glyco:protein IIB or IIIa and thrombin inhibitory | Wolfields. | For treating thrombotic diseases, atherosclerosis, | Wolfields. | Wolfields
formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 ö
 (BIOJ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
Blifunctional inhibitors of thrombin and platelet activation comprise 91yco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis,
 Score 261; DB 5; Length 97;
Pred. No. 2.74e-17;
10; Mismatches 19; Indels
 T 15
R25149 standard; Protein; 99 AA.
 51.6%;
 30; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 Best Local Similarity
 97 AA;
 WO9210575-A.
 Sequence
 Query Match
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SQ Sequence 99 AA;

Query Match 51.6%; Score 261; DB 5; Length 99; Best Local Similarity 50.8%; Pred. No. 2.74e-17; Matches 30; Conservative 10; Mismatches 19; Indels 0; Gaps

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Search completed: Fri Sep 25 13:18:10 1998 Job time : 19 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 4.89 Seconds 221.602 Million cell updates/sec MPsrch\_pp

Fri Sep 25 13:19:54 1998; Run on:

>PCT-US98-16719-20 (1-67) from PCTUS9816719A.pep 508 Description: Perfect Score:

Tabular output not generated.

NSVHPCCDPVXCEPREGEHC......DYCTGISXDCPRNRYKGKED Sequence:

67

PAM 150 Gap 11 Scoring table:

131922 seqs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq32 Database:

|:paril'2:part2 3:part3 4:part4 5:part5 6:part6 7:part3 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part29 23:part24 25:part25 26:part26 27:part27 28:part28 29:part29

Mean 24.765; Variance 93.857; scale 0.264 tatistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | 88 | QI     | Description           | Pred. No. |
|---------------|-------|----------------|--------------------------|----|--------|-----------------------|-----------|
| 1             | 283   | 55.7           | 73                       | 23 | W14083 | Platelet aggregation  | 4.02e-20  |
| 7             | 274   | 53.9           | 73                       | 7  | R06494 | Platelet addredation  | 3.62e-19  |
| m             | 274   | 53.9           | 480                      | œ  | R42867 | Platelet aggregation  | 3.62e-19  |
| 4             | 263   | 51.8           | 97                       | Ŋ  | R28708 | Bifunctional inhibito | 5.28e-18  |
| 2             | 263   | 51.8           | 86                       | 'n | R25154 | Bifunctional inhibito | 5.28e-18  |
| φ             | 262   | 51.6           | 71                       | 10 | R53942 | Disintegrin peptide # | 6.73e-18  |
| 7             | 259   | 51.0           | 96                       | ഹ  | R28707 | Bifunctional inhibito | 1.40e-17  |
| 60            | 259   | 51.0           | 97                       | 'n | R28706 | Bifunctional inhibito | 1.40e-17  |
| σ             | 259   | 51.0           | 66                       | ស  | R25153 | Bifunctional inhibito | 1.40e-17  |
| 10            | 259   | 51.0           | 106                      | S  | R25152 | Bifunctional inhibito | 1.40e-17  |
| 11            | 257   | 50.6           | 97                       | Ŋ  | R28705 | Bifunctional inhibito | 2.27e-17  |
| 12            | 257   | 50.6           | 86                       | 'n | R25150 | Bifunctional inhibito | 2.27e-17  |
| 13            | 256   | 50.4           | 72                       | ო  | R10109 | Trigramin-beta 1      | 2.89e-17  |
| 14            | 256   | 50.4           | 73                       | m  | R10110 | Trigramin-beta 2.     | 2.89e-17  |
| 15            | 255   | 50.2           | 96                       | 'n | R25382 | Bifunctional inhibito | 3.68e-17  |
| 16            | 255   | 50.2           | 96                       | S  | R25151 | Bifunctional inhibito | 3.68e-17  |
| 17            | 253   | 49.8           | 47                       | ო  | R10113 | Echistatin-alpha 2.   | 5.98e-17  |
| 18            | 253   | 49.8           | 49                       | m  | R12986 | Echistatin fibrinogen | 5.98e-17  |

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4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNYK 62

g ó R06494 standard; protein; 73 AA.
R06494.
R04-JAN-1991 (first entry)
Platelet aggregation inhibitor.
Snake venom; thromboxan A2; thrombosis; anti-coagulant.

RESULT

ME DA S

|                       |        |        | _      |          |                       |                       |        |        |          |                       |                       |                       |                       |                  |             |        |         |        |          |        |                       |                       |          |          |          |
|-----------------------|--------|--------|--------|----------|-----------------------|-----------------------|--------|--------|----------|-----------------------|-----------------------|-----------------------|-----------------------|------------------|-------------|--------|---------|--------|----------|--------|-----------------------|-----------------------|----------|----------|----------|
| 5.98e-17              | . 98e- | .98e-  | .98e-  | .62e-1   | .58e-1                | .58e-1                | .58e-1 | .58e-1 | 1.58e-16 | .58e-1                | .58e-1                | .01e-1                |                       | .01e-1           | .01e-1      | e-1    | .56e-16 | .26e-1 | 3.26e-16 | .26e-1 | .15e-1                | .72e-1                | 6.72e-16 | .09e-1   |          |
|                       |        |        |        |          |                       |                       |        |        |          |                       |                       |                       |                       | .,               | .,          |        |         |        |          | ٠,     | -                     | _                     |          |          |          |
| Sequence of viper ven |        | -      | onal   | adheston | Platelet adhesion blo | Example of cysteine-r | ö      |        | ad       | Disintegrin peptide # | Bifunctional inhibito | Albolabrin peptide ta | Disintegrin peptide # | Trigramin-gamma. | Albolabrin. |        | ō       | oŧ     | rin      | ~      | New trigramin peptide | Echistatin with Asp o | VID      | of viper | of viper |
|                       |        |        |        |          |                       |                       |        |        |          |                       |                       |                       |                       |                  |             |        |         |        |          |        |                       |                       |          |          |          |
| P91098                | R28704 | R25149 | R25148 | m        | R24287                | ~                     | W02647 | 8      | 8        | R53938                | R25147                | 8                     | R53946                | R10106           | R06395      | P91095 | P91100  | P91099 | R53940   | R06396 | P91320                | 342                   | P91094   | 0        | P91096   |
| 4 N                   | 'n     | S      | Ŋ      | ~        | ~                     | н                     | 18     | 4      | ~        | 20                    | S                     | 28                    | 2                     | ٣                | ~           | 4      | 4       | 7      | 2        | ~      | -                     | ø                     | 7        | 4        | 4        |
| 4 c                   | 93     | 66     | 106    | 49       | σ                     |                       | 6      | 49     | 49       | 49                    | 96                    | •                     | 73                    | 73               | 73          | 49     | 49      |        |          |        |                       | σ                     | 49       |          | 49       |
| 49.8                  | . 6    |        | ٠      | 49.6     | •                     | 49.0                  | 49.0   | 49.0   | 49.0     | 49.0                  | 49.0                  |                       | 48.8                  | ъ.               | ٠           |        | 48.6    | 48.4   | 48.4     | 48.4   | 48.2                  | 47.8                  | ٠        | 47.4     | 46.5     |
| 253                   | S      | S      | S      | n        | 249                   | 4                     | 4      | 249    | 4        | 249                   | 249                   | 248                   | 248                   | 248              | 248         | 247    | 247     | 246    | 246      | 246    | 245                   | 243                   | 243      | 241      | m        |
| 19                    | 21     | 22     | 23     | 24       | 25                    | 56                    | 27     | 78     | 53       | 30                    | 31                    | 32                    | 33                    | 34               | 35          | 36     | 37      | 38     | 39       | 40     | 41                    | 42                    | 43       | 44       | 45       |

#### ALIGNMENTS

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D 10-JAN-1997 D 10-JAN-1997 D 10-JAN-1997 D 10-JAN-1995 D 10-JAN-1995 D 10-JAN-1995 D 10-JAN-1995 D 10-JAN-1995 D 10-JAN-1995 KR-019685.

ROS-JUL-1995; KR-019685.

MAKI-) ZH MAKINA SEIMEI KOGAKU KENKYUSHO.

DOO SK, HaX DK, Hong MM, IN CK, Jeong HY, Kwang HC;

SOO JL, Yung DY;

WPI; 97-121376/12.

PEPtide derived from Korean salmosa viper venom - useful as blood partielet aggregation inhibitor, for the management of thrombosis claim i; Page 11; 15pp; French.

This peptide, designated Salmosin, inhibits blood platelet aggregation.

It is derived from the venom of the Korean salmosa viper (Agkistrodon till selvent and the venom of the management of thrombosis. Salmosin also has higher activity than control of thrombosis. Salmosin also has higher activity than and echistatin.
 W14083;
27-007-1997 (first entry)
Platelet aggregation inhibitor, Salmosin.
Salmosin; Inhibit; blood; platelet aggregation; venom; Korean;
salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.
FR2736266-Al.
 Gaps
 .;
0
 Score 283; DB 23; Length 73;
Pred. No. 4.02e-20;
10; Mismatches 19; Indels
Jr 1
W14083 standard; peptide; 73 AA.
 Query Match 55.7%;
Best Local Similarity 50.8%;
Matches 30; Conservative
 73 AA;
 Sequence
RESULT
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PD 25-JUN-1992.

W 25-JUN-1992.

D5-DEC-1991; U09108.

R 07-DEC-1991; U09108.

R 07-DEC-1991; U09108.

PR 07-DEC-1991; U09108.

PA (BIOJ) BIOGEN INC.

Chao BH, Maraganore JM, Strauch KL, Thompson JS;

WF1: 92-24650/28.

D8 WF1: 92-24650/28.

D8 WF1: 92-24650/28.

D8 WF1: 92-24650/28.

D8 WF1: 92-24650/28.

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D8 WF1: 92-24650/28.

D8 WF1: 92-24650/28.

Comprise glyco: protein INB of INI and thrombin inhibitory in the inhibitor of platelet and is referred to as C-appilog(lead!).

CT he inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is transfer myocardial infarction, or thromboslytic agent such as the decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 (BIOJ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WHI; 92-34660/28.
Bl:functional inhibitors of thrombin and platelet activation -
comprise glyco:protein IIB or IIIa and thrombin inhibitory
moieties, for treating thrombotic diseases, atherosclerosis,
cancer and neuro:degenerative conditions
Claim 7; Page 25; 103pp; English.
This sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as IIe-Met-C-appilog(leu41)
The inhibitor also contains a thrombin inhibiting component. The
inhibitor is used to inhibit thrombin and platelet-mediated processes
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #13.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 04-JAN 1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #14.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 14 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpfh 73
 Score 263; DB 5; Length 97;
Pred. No. 5.28e-18;
8; Mismatches 22; Indels
 .T 5
R25154 standard; Protein; 98 AA.
 Query Match 51.8%;
Best Local Similarity 50.8%;
Matches 31; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 97 AA;
 Synthetic.
WO9210575-A.
 Synthetic.
 G 64
 74 9 74
 Sequence
 R25154;
 64
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 420 npccdaatcklrggagcaeglccdqcrfmkkgtvcriargddmddycngisagcprnpf 478
 Gaps
 0; Gaps
 and new recombinant DNA ancoding it.

Claim 3; Fig 9; 73pp; English.

The sequence is deduced from the coding strand of a synthetic gene for a polypeptide inhibitor of platelet activation. The polypeptide is analogous to that obtd. from the venom of Agkistrodon p. piscivorus (North American Water Moccasin). The gene can be used to produce recombinant inhibitor or fusion proteins with eq. hirudin derivs. These can be used to decrease/inhibit platelet aggregation and release in vivo or in vitro.

Usual dose is 0.01-100 mg/Kg body wt. The recombinant protein can also be used to coat the surfaces of invasive medical devices.
 Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example; Page 33-35; 50pp; Japanese.

The sequence is that of a polypeptide which inhibits platelet
 Pure platelet activation inhibiting polypeptide from snake venom - used for preventing agglutination and release in vivo or vitro,
 The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid
 can also block stenosis and spasm at the site of thrombosis
 ;
0
 11-MAY-1994 (first entry)
platelet aggregation inhibitory peptide.
Inhibition: ADP: collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
 Score 274; DB 8; Length 480; Pred. No. 3.62e-19; 12; Mismatches 19; Indels
 Score 274; DB 2; Length 73;
Pred. No. 3.62e-19;
9; Mismatches 20; Indels
 (by inhibiting the release of thromboxan A2). See also R06508.
 Maraganore JM, Jakubowski JA, Chao BH;
WPI; 90-260891/34.
N-PSDB; Q05730.
 .T 3
R42867 standard; Protein; 480 AA.
 RESULT 4
ID R28708 standard; Protein; 97 AA
 03-007-1991; 256234.
26-007-1990; JP-287116.
20-FBB-1991; JP-0285328.
(TAKE) TAKEDA CHEM IND LID.
WPI; 93-348481/44.
 53.9%;
 Query Match
Best Local Similarity 47.5%;
Matches 28; Conservative
 30; Conservative
 26-JAN-1990; U00465.
27-JAN-1989; US-303590.
27-JAN-1989; US-303585.
01-NOV-1989; US-430313.
(BIOG) BIOGEN INC.
(UXBO-) BOSTON UNIV.
 Best Local Similarity
Matches 30; Conserv
 480 AA;
 N-PSDB; Q50394
 J05255395-A.
 09-AUG-1990
 05-0CT-1993
 Sequence
 Query Match
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 Radio-labelled polypeptide(s) derived from viperidae
disintegrin(s) - for treatment and diagnosis of venous and
atterial thrombi, pulmonary emboli and tumours or abscesses
having a thrombus component.

Claim 24; Page 46; 62pp; English.

C The sequences given in R59333 46 are disintegrin peptides.

C The sequences given in R59333 46 are disintegrin peptides.

C India 24; Page 46; 62pp; English.

C The sequences given in R59333 46 are disintegrin peptides.

C India 24; Page 46; 62pp; English.

C India 24; Page 46; Pa
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in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thromboals; increase resocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 R28707 standard; Protein; 96 AA. R28707; 04-73N-1993 (first entry) Bifunctional inhibitor of platelet activation and thrombin #11. Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction;
 15 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpfh 74
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRYK 63
 Gaps
 Gaps
 13 npccdaatcklrpgaqcaqglccdqckfmkegtvcr-argddvndycngisagcprnpf 70
 Disintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen; integrin binding sites; GP IIb/IIIa; human; platelets; radiolabel; treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;
 Score 262; DB 10; Length 71;
Pred. No. 6.73e-18;
9; Mismatches 19; Indels 1;
 pulmonary emboli and
 ;;
 Length 98;
 22; Indels
 tumours or abscesses that have a thrombus component
Sequence 71 AA;
 Score 263; DB 5; 1
Pred. No. 5.28e-18;
 8; Mismatches
 diagnosis of venous and arterial thrombi,
 thrombus component.
 standard; peptide; 71 AA.
 Query Match
Best Local Similarity 50.8%;
Matches 30; Conservative
 Query Match 51.8%;
Best Local Similarity 50.8%;
Matches 31; Conservative
 21-DEC-1994 (first entry)
Disintegrin peptide #10.
 Agkistrodon piscivorous.
 05-OCT-1993; U09523.
19-OCT-1992; US-965674.
(UTEM) UNIV TEMPLE.
 t LC, Maurer AH;
94-151248/18.
 tumours; abscesses;
 28-APR-1994
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 Sequence
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Chao BH. Maraganore JM. Strauch KL, Thompson JS;
WRI: 92-234630/28
WRI: 92-234630/28
WRI: 92-234630/28

Bifunctional inhibitors of thrombin and platelet activation -
comprise glyco:protein IIB or IIIa and thrombin inhibitory
moieties, for treating thrombotic diseases, atherosclerosis,
cancer and neuro:degenerative conditions
Claim 7: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 5: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: English.
Claim 6: Page 24: 103pp: English.
Claim 7: Page 24: 103pp: 103
 moleties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions
claim 7: Page 24: 103pp; English.
This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as C-appilog. The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extraocoporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombotycopenia. The usual dose is lug-5mg/Kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat
 4 HPCCDDVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRYK 63
 13 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpfh 72
 clot;
 Gaps
thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #10.
Bifunctional inhibitor; platelet activation; thrombin; inhibit of formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion;
 ö
 WPI; 92-234630/28.
Bi:functional inhibitors of thrombin and platelet activation
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moleties, for treating thrombotic diseases, atherosclerosis,
 9; Mismatches 22; Indels
 5; Length 96;
 Chao BH, Maraganore JM, Strauch KL, Thompson JS;
 Score 259; DB 5; Pred. No. 1.40e-17;
 time; inhibiting metastatic cell growth.
 T 8
R28706 standard; Protein; 97 AA.
 Query Match
Best Local Similarity 49.2%;
 Conservative
 05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 US-623611.
 05-DEC-1991; U09108.
07-DEC-1990; US-6236
(BIOJ) BIOGEN INC.
 (BIOJ) BIOGEN INC.
 Synthetic.
WO9210575-A.
25-JUN-1992.
 30;
 25-JUN-1992.
 73 g 73
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83 g 83
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 Claim 7; Page 24; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as Ala-Asn-Ser-C-appilog The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombolis; increase recolusion
 prevent myocardial infarction, or thrombosis; increase reocclusion
 04-JAN'1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #12.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion;
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFINAGTICKXAMLDGLNDYCTGISXDCPRNRYK 63
 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpfh 73
 npcddaatcklrpgagcaeglccdgckfmkegtvcrrargddvndycngisagcprnpfh 75
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #9.
bifunctional inhibitor; platelet activation; thrombin; inhibit clot;
 Gaps
 decreasing reperfusion time: and inhibiting metastatic cell
h. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 decreasing reperfusion time; and inhibiting metastatic cell n. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.nce 99 AA;
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 Bi:functional inhibitors of thrombin and platelet activation
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis,
 Score 259; DB 5; Length 99;
Pred. No. 1.40e-17;
9; Mismatches 22; Indels
 Score 259; DB 5; Length 97;
Pred. No. 1.40e-17;
9; Mismatches 22; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
 cancer and neuro: degenerative conditions
 time; inhibiting metastatic cell growth
 R25152 standard; Protein; 106 AA. R25152;
 T 9
R25153 standard; Protein; 99 AA.
 51.0%;
ilarity 49.2%;
Conservative
 Similarity 49.2%;
30; Conservative
 07-DEC-1990; US-623611.
 25-JUN-1992.
05-DEC-1991; U09108.
 (BIOJ) BIOGEN INC.
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 74 g 74
 G 64
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 Synthetic
 Sequence
 Sequence
 growth.
 growth.
 R25153;
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inhibitor is used to inhibit thrombin and platelet mediated processes in patients or in extracorporeal blood. It inhibits clot formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
 claim 5; Page 24; 103pp; English.
This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as N-appilog(LeuG5).
The inhibitor also contains a thrombin inhibiting component. The inhibitor is used to inhibit thrombin and platelet-mediated processes in patients or in extracorporal blood. It inhibits call formation and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopaenia. The usual dose is
 MR8705;
04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #7.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot;
formation; accretion; fibrin deposition; myocardial infarction;
formation; increasing reocclusion time; decreasing reperfusion;
time; inhibiting metastatic cell growth.
 + HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRYK 63
 Gaps
 23 npcddaatcklrpgaqcaeglccdqckfmkegtvcrrargddvndycngisagcprnpfh
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis, cancer and neuro:degenerative conditions claim 7; Page 24; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet activation and thrombin, and is referred to as Gly-Ser-Ile-Glu-Gly-Arg-Pro-Glu-Phe-Met-C-appilog
The inhibitor also contains a thrombin inhibiting component. The
 reperfusion;
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 myocardial infarction;
 Bi:functional inhibitors of thrombin and platelet activation
 Bi:functional inhibitors of thrombin and platelet activation
 comprise glyco:protein IIB or IIIa and thrombin inhibitory moieties, for treating thrombotic diseases, atherosclerosis,
 DB 5; Length 106;
 22; Indels
 decreasing
 (BIOJ) BIOGEN INC.
Chao BH, Maraganore JM, Strauch KL, Thompson JS;
WPI; 92-234630/28.
 Chao BH, Maraganore JM, Strauch KL, Thompson JS;
 Score 259; DB 5;
Pred. No. 1.40e-17;
 9; Mismatches
formation; accretion; fibrin deposition;
thrombosis; increasing reocclusion time;
time; inhibiting metastatic cell growth.
Synthetic.
 cancer and neuro:degenerative conditions
 standard; Protein; 97 AA.
 Query Match 51.0%;
Best Local Similarity 49.2%;
Matches 30; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 (BIOJ) BIOGEN INC.
 106 AA;
 92-234630/28
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13-MAR-1991
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 Sequence
 Query Match
 70 pf
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 R10110;
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 comprise glyco:protein IIB or III and thrombin inhibitory
moleties, for treating thrombotic diseases, atherosclerosis,
claim 5; Page 23; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as Ile-Met-N-appliog(Leu65)
crimis sequence represents the bifunctional inhibitor of platelet
activation and thrombin, and is referred to as Ile-Met-N-appliog(Leu65)
The inhibitor also contains a thrombin inhibiting component. The
inhibitor is used to inhibit thrombin and platelet-mediated processes
in patients or in extracorporaal blood. It inhibits clot formation
and growth caused by platelets and clot accretion caused by fibrin
deposition, but do not cause thrombocytopaenia. The usual dose is
tissue plasminogen activator. The inhibitor may be used to treat
or prevent myocardial infarction, or thrombosis; increase reocclusion
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lug-5mg/kg/day opt. combined with a thrombolytic agent such as tissue plasminogen activator. The inhibitor may be used to treat or prevent myocardial infarction, or thrombosis; increase reocclusion time; decreasing reperfusion time; and inhibiting metastatic cell growth. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80. Sequence 97 AA;
 04-JAN-1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #6.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 Gaps
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpf 97
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 38 npcddaatcklrpgaqcaeglccdqckflkegtvcrrargddvndycngisagcprnpf 96
 decreasing reperfusion time; and inhibiting metastatic cell
h. See also R25142-54 R25382,3, Q25314,5 Q25884-90, Q31179,80.
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 ö
 Bi:functional inhibitors of thrombin and platelet activation
 Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition; GP IIA; GP IIIA; hypercoagulation.
 Score 257; DB 5; Length 97; Pred. No. 2.27e-17;
 Length 98;
 8; Mismatches 21; Indels
 Score 257; DB 5; Length 98; Pred. No. 2.27e-17; 8; Mismatches 21; Indels
 Chao BH, Maraganore JM, Strauch KL, Thompson JS; WPI; 92-234630/28.
 standard; Protein; 98 AA.
 R10109 standard; Protein; 72 AA. R10109 13-MAR-1991 (first entry) rilgramin-beta 1
 50.6%;
llarity 50.8%;
Conservative
 / Match 50.6%;
Local Similarity 50.8%;
nes 30; Conservative
 25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
 13-DEC-1990.
07-JUN-1990; U03216.
07-JUN-1989; US-362718.
 BIOJ) BIOGEN INC.
 Local Similarity
nes 30; Conser
 98 AA;
 R25150 8 R25150;
 Sequence
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 time;
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 04-JAN'1993 (first entry)
Bifunctional inhibitor of platelet activation and thrombin #15.
Bifunctional inhibitor; platelet activation; thrombin; inhibit clot; formation; accretion; fibrin deposition; mycardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
 10 spanpccdaatckllpgaaqcgegpccdqcsfmkkgticrrargddlddycngrsagcprn 69
 10 spanpccdaatckllpgaqcgegpccdqcsfmkkgt1crrargdd1ddycngrsagcprn 69
 Gaps
 Gaps
 IIA-GP IIIA.

Disclosure, Fig 11; 91pp; English.

The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.

See also R10106-R10113

Sequence 72 AA;
 Disclosure; Fig 11; 91pp; English.
The sequence was determined by Edman degradation. Synthetic genes based on the sequence can be used to express recombinant trigramin protein for treatment of hypercoagulation-related states.
 ö
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 GР
 g
 Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition; GP IIIA; dP IIIA; hypercoagulation.
 Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to IIA-GP IIIA.
 Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to
 Score 256; DB 3; Length 73;
Pred. No. 2.89e-17;
10; Mismatches 23; Indels
 Score 256; DB 3; Length 72;
Pred. No. 2.89e-17;
10; Mismatches 23; Indels
 T 15
R25382 standard; Protein; 96 AA.
 T 14
R10110 standard; Protein; 73 AA.
 50.4%;
llarity 46.8%;
Conservative
 Best Local Similarity 46.8%;
Matches 29; Conservation
 (first entry)
 13-DEC-1990.
07-JUN-1990; U03216.
07-JUN-1989; US-362718.
(GETH) GENENTECH INC.
Lazarus RA, Dennis MS;
WPI; 91-007159/01.
 See also R10106-R10113
 Lazarus RA, Dennis MS;
WPI; 91-007159/01.
 Best Local Similarity
Matches 29; Conser
 Trigramin-beta 2
 WO9015072-A.
 R25382;
04-JAN-1993
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Chao BH. Maraganore JM. Strauch KL, Thompson JS;

WID JDECTROYS US-625011.

Chao BH. Maraganore JM. Strauch KL, Thompson JS;

WHI; 92-234630/2B.

BH:functional inhibitors of thrombin and platelet activation -

BH:functional inhibitors of thrombin inhibitory

Comprise glyco:protein IIB or IIIa and thrombin inhibitory

moieties, for treating thrombotic diseases, atherosclerosis,

cancer and neuro:degenerative conditions

Claim 9a: Page 76; 103pp; English.

This sequence represents the bifunctional inhibitor of platelet activation. The inhibit for also contains a thrombin inhibiting component.

It is used to inhibit thrombin and platelet-mediated processes

It is used to inhibit thrombin and platelet-mediated processes

It is used to inhibit thrombin and platelet accretion caused by fibrin and growth caused by platelets and clot accretion caused by fibrin deposition, but do not cause thrombocytopeania. The usual dose is

tissue plasminogen activator. The inhibitor may be used to treat

or prevent myocardial infarction, or thrombosis; increase reocclusion

time; decreasing reperfusion time; and inhibiting metastatic cell

Sequence 96 AA;
Synthetic.
W09210575-A.
25-JUN-1992.
05-DEC-1991; U09108.
07-DEC-1990; US-623611.
```

ö 13 npcddaatcklrpgaqcaeglccdqckfxkegtvcrrargddvndycngisagcprnpfh 72 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRYK 63 Gaps Score 255; DB 5; Length 96; Pred. No. 3.68e-17; 8; Mismatches 23; Indels Query Match 50.2%; Best Local Similarity 49.2%; Matches 30; Conservative g ò

73 g 73 g

64 G 64

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Search completed: Fri Sep 25 13:20:12 1998 Job time : 18 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 4.69 Seconds 358.415 Million cell updates/sec Fri Sep 25 13:18:28 1998; Run on:

Tabular output not generated.

>PCT-US98-16719-20 (1-67) from PCTUS9816719A.pep 508 1 NSVHPCCDPVXCEPREGEHC......DYCTGISXDCPRNRYKGKED 67 Title: Description: Perfect Score: Sequence:

Scoring table:

69111 segs, 25083644 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot35 1:swissl Database:

scale 0.640 Mean 34.300; Variance 53.615; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|            | Pred. No.       | 1.33e-44    | 6.48e-42    | 3.26e-40    | 1.74e-39    | 9.24e-39    | 1.61e-38    | 2.81e-38    | 2.81e-38    | 8.53e-38    | 8.53e-38    | 8.53e-38    | 1.49e-37               | 7.84e-37    | 4.12e-36    | 1.25e-35    | 3.39e-34    | 3.39e-34    | 1.02e-33    | 1.02e-33    | 1.02e-33    | 4.71e-32    | 2.42e-31    | 4.17e-31    |
|------------|-----------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
|            |                 | HALYSIN (P  | APPLAGIN (  | TRIGRAMIN   | ECHISTATIN  | VIRIDIN (P  | CEREBERIN   | TRIGRAMIN   | MOLOSSIN (  | BATROXOSTA  | COTIARIN (  | JARARACIN   | IOM METALLO            | BASILICIN   | LACHESIN (  | METALLOPRO  | TERGEMININ  | BARBOURIN   | CROTATROXI  | LUTOSIN (P  | CERASTIN (  | ERISTICOPH  | (CYTOTOXIC  | FLAVOSTATI  |
|            | Description     | DISINTEGRIN | PUTATIVE VENOM METALLO | DISINTEGRIN | DISINTEGRIN | HEMORRHAGIC | DISINTEGRIN |
|            | ΙD              | DISLAGKHA   | DISI_AGKPI  | DISB_TRIGA  | DISI_ECHCA  | DISI_CROVV  | DISI_CROVE  | DISG_TRIGA  | DISI_CROMM  | DISI_BOTAT  | DISI_BOTCO  | DISI_BOTJA  | DISA_TRIGA             | DISI_CROBA  | DISI_LACMU  | HRTE_CROAT  | DISI_SISTE  | DISI_SISBA  | DISI_CROAT  | DISI_CROVL  | DISI_CROCC  | DISI_ERIMA  |             | DISI_TRIFL  |
|            | 80              | -           | -           | Н           | Н           |             | -           | Н           | н           | -           | -           | -           | Н                      | -           | Н           | ч           | Н           | Н           |             | Н           | н           | -           | -           | -           |
|            | Match Length DB | 7.1         | 71          | 73          | 49          | 71          | 72          | 73          | 73          | 71          | 72          | 73          | 480                    | 72          | 73          | 478         | 73          | 73          | 72          | 73          | 73          | 51          | 75          | 68          |
| &<br>Ouerv | Match           | 53.9        | 51.8        | 50.4        | 49.8        | 49.2        | 49.0        | 48.8        | 48.8        | 48.4        | 48.4        | 48.4        | 48.2                   | 47.6        | 47.0        | 46.7        | 45.5        | 45.5        | 45.1        | 45.1        | 45.1        | 43.7        | 43.1        | 42.9        |
|            | Score           | 274         | 263         | 256         | 253         | 250         | 249         | 248         | 248         | 246         | 246         | 246         | 245                    | 242         | 239         | 237         | 231         | 231         | 229         | 229         | 229         | 222         | 219         | 218         |
| Result     | No.             | -           | 7           | m           | 4           | S           | ø           | 7           | <b>œ</b>    | σ           | 10          | 11          | 12                     | 13          | 14          | 15          | 16          | 17          | 18          | 19          | 50          | 21          | 22          | 23          |
|            |                 |             |             |             |             |             |             |             |             |             |             |             |                        |             |             |             |             |             |             |             |             |             |             |             |

ID DISI\_AGKPI STANDARD; PRT; 71 AA.

AC P16338;
DT 01-AGG-1990 (REL. 15, CREATED)
DT 01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-BCC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE DISINTEGRIN APPLAGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
OS AGKISTRODON PISCIVORUS PISCIVORUS (EASTERN COTTONMOUTH).

| ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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| 17e-31<br>24e-30<br>24e-30<br>26e-29<br>62e-28<br>62e-28<br>67e-25<br>18e-24<br>67e-25<br>67e-25<br>67e-25<br>67e-27<br>67e-04<br>73e-04<br>73e-04<br>73e-03<br>73e-02<br>73e-02<br>73e-03<br>73e-03<br>73e-03<br>73e-03<br>73e-03<br>73e-03                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | OR). A: A: RECEPTORS ING IO THE IND INHIBIT IG FACTOR : VENOM.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Gaps<br>F 71<br>: 62                                                                                                                                                                         |
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Score 274; DB 1; Length 71; al Similarity 47.5%; Pred. No. 1.33e-44; 28; Conservative 12; Mismatches 19; Indels 0; G NPCCDAATCKLROGAQCAEGLCCDQCREMKKGTVCRIARGDDMDDYCNGISAGCPRNPF: |
| TEGRIN TE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | A.  TE)  ACTIVATIO  TETRAPODA  CM.;  ION WITH  PLEX. ACT  PLATELET  PLATELET  IIB-IIIA  IS FOUND  ; VENOM.  T SITE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 19;<br>19;<br>DDMI                                                                                                                                                                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 71 AA.  DDATE) UPDATE) (ION ACTI TA: TETH TA: TETH TACTION THE PLAN IIN, PLAN IIN, PLAN IN, PLAN SISION; VE SISION; VE CRINEEN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 274; DB 1;<br>No. 1.33e-4<br>Mismatches<br>MKKGTVCRIARG<br>::   : :  <br>ILNAGTICKXAML                                                                                                       |
| DISI_TRIEL DISI_AGRRH DISR_AGRRH DISS_BITAR DISI_BITAR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ALIGNMENTS  1 2.4GKHA STANDARD; PRT; 71 AA.  1518.  1AY-1991 (REL. 18, CREATED)  1AY-1992 (REL. 24, LAST SEQUENCE UPDATE)  1AY-1992 (REL. 24, LAST ANNOTATION ACTIVATION  1AY-1992 (REL. 24, LAST ANNOTATION ACTIVATION  1AY-1992 (REL. 24, LAST ANNOTATION ACTIVATION  1AY-1992 (REL. 1209-1219(1991).  1AY-1994 (ASTACOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET STANDENSESSED ON GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET STANDENSESSED ON GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET STANDENSING (ASTACOPROTEIN IIB-IIIA PISTRESSED ON GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET STANDENSING (ASTACOPROTEIN)  1AND COLLEGEN  1. PANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND:  1. THAT IS SEGORATION; PLATELET; CELL ADHESION; VENOM.  1. LEID 47 66  2. SIMILARITY.  1. SA CELL ATTACHENT SITE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Score 274;<br>Pred. No.<br>12; Misma<br>CDQCRFMKKGT'<br>   : ::  <br>CRNCKFLNAGT                                                                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ALI  (D;  CREATED)  LAST SEC  LAST SEC  LAST AND  CREATED  LAST AND  COUNTAINS  S.  COUYANG   | .9%;<br>.5%;<br>.ive<br>.AEGLC                                                                                                                                                               |
| 2 8 8 3 4 4 6 8 8 8 4 4 6 8 8 8 8 2 4 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Z BY ZIG CHUB E. BY 218 Z                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 53.9% arity 47.5% Conservative CKLRQGAQCAEG                                                                                                                                                  |
| 2444<br>4422<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135<br>441135 | 1. ALL STANDARD; 58; AY-1991 (REL. 18, LAST ANA-1991 (REL. 18, LAST ANA-1991 (REL. 18, LAST ANA-1991 (REL. 18, LAST ANA-1992 (REL. 14, LAST ANA-1992 (REL. 24, LAST ANA-1993 (REL. 24, LAST ANA-1993 (REL. 21, LUU CS., OUYAN HEM. PHARMACOL. 42:1209-11 (RE. PROPERTY) (RELEDINGED BY ADA-1993 (REL. 1993) (REL. 1993) (REL. 1994) (REL   | Similarity<br>28; Conse<br>CDAATCKLRQ<br>  :    :                                                                                                                                            |
| 224<br>225<br>226<br>226<br>227<br>220<br>221<br>221<br>221<br>221<br>221<br>233<br>333<br>333<br>333<br>333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | REAL SECOND SECO | Query<br>Best<br>Match<br>Db<br>Oy                                                                                                                                                           |

Length 73;

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(CARINATIN)
 62
 DISI_ECHCA
 70 PF 71
 DISULFIDE
 SEQUENCE
 SEQUENCE
 Query Match
 61 RY
 Matches
 RESULT
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 MEDLINE; 90207217.

DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DESHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).

-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROPTEN IIB-IIIB-IIIS COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPPOR ON THE PLATELET SUBFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 CHAO B.H., JAKUBGWSKI J.A., SAVAGE B., PING CHOW E., MARZEC U.M., HARKER L.A., MARAGANORE J.M.;
PROC. NATL. ACAD. SCI. U.S.A. 86:8050-8054(1989).
-! FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
-! EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 Gaps
 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 NPCCDAATCKLRPGAQCAEGICCDQCKFMKEGTVCR-ARGDDVNDYCNGISAGCPRNPF 70
 (GREEN HABU SNAKE)
 AND COLLAGEN.

THE SEQUENCE SHOWN IS THAT OF TRIGRAMIN BETA-2.

SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS. CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
C35982; C35982.
 -!- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR, A33990, A33990,
HSSP; P1494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SIGUEND 47 65 BY SIMILARITY.
SITE 50 52 CELL ATTACHMENT SITE.
SEQUENCE 71 AA; 7522 MW; 320595A1 CRC32;
 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ÷
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPIILIA;
LEPIDOSAURIA; SERPENTES.
 01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DISINYEGRIN TRICRAMIN BETA (PLATELET AGGREGATION ACTIVATION
 Score 263; DB 1; Length 71;
Pred. No. 6.48e-42;
9; Mismatches 19; Indels
 N; PLATELET; CELL ADHESION; VENOM.

15 BY SIMILARITY.

35 BY SIMILARITY.

59 BY SIMILARITY.

58 BY SIMILARITY.

66 BY SIMILARITY.

53 CELL ATTACHENTY.

53 MISSING (IN BETA-1 FORM).

7633 MW; 61CBAFCF CRC32;
 TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER)
 73 AA
 PRT;
 HSSP; P17494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
 Query Match 51.8%;
Best Local Similarity 50.8%;
Matches 30; Conservative
 STANDARD;
 BLOOD COAGULATION;
 90046735
 AND COLLAGEN.
 73
 TISSUE-VENOM;
 T 3
DISB_TRIGA
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 SEQUENCE
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 SEQUENCE
 DISULFID
 DISULFID
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 VARIANT
 PIR;
 13
 RESULT
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 10 SPANPCCDAATCKLLPGAQCGEGPCCDQCSFMKKGTICRRARGDDLDDYCNGRSAGCPRN 69
 Gaps
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 STRUCTURE BY NMR.
MEDLINE; 92104121.
COOKE R.M., CARTER B.G., MARTIN D.M.A., MURRAY-RUST P., WEIR M.P.;
EUR. J. BIOCHEM. 202:323-328(1991).
 01-AUG-1990 (REL. 15, CREATED)
1-EBE-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANOTATION UPDATE)
DISINTEGRIN ECHISTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
 GAN Z.R., GOULD R.J., JACOBS J.W., FRIEDMAN P.A., POLOKOFF M.A.;
J. BIOL. CHEM. 263:19827-19832(1988).
 MEDLINE; 92104150.
DALVIT C., WIDMER H., BOVERMANN G., BRECKENRIDGE R., METTERNICH EUR. J. BIOCHEM. 202:315-321(1991).
 MEDLINE; 90207217.
DEDNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
 MEDLINE; 92089067.
CHEN Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL G.,
BADM J.;
 ö
 EUKARYOTA; METAZÓA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 23; Indels
 P., PELTON J.T.;
Score 256; DB 1; 1
Pred. No. 3.26e-40;
10; Mismatches 23,
 49 AA
 MEDLINE; 91308124.
SAUDEK V., ATKINSON R.A., PELTON J.T.;
BIOCHEMISTRY 30:7369-7372(1991).
 SAUDEK V., ATKINSON R.A., LEPAGE P. EUR. J. BIOCHEM. 202:329-338(1991).
 PRT;
 ECHIS CARINATUS (SAW-SCALED VIPER)
 BIOCHEMISTRY 30:11625-11636(1991).
50.4%;
Similarity 46.8%;
29; Conservative
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 Best Local Similarity
 TISSUE-VENOM;
MEDLINE; 89066819.
 MEDLINE; 92104152
 STRUCTURE BY NMR
 STRUCTURE BY NMR
 STRUCTURE BY NMR
 STRUCTURE BY NMR
 LISSUE=VENOM;
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MEDLINE; 9112315.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARRSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-I- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA ROMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
 -i-SIMILARITY DELONGS TO THE FAMILY OF GPILB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PRIS, B43020, B43020,
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ATTACHMENT SITE (POTENTIAL).
SITE 51 SA CREL ATTACHMENT SITE (POTENTIAL).
 SPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 69
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN CEREBERIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CONTALUS VIRIDIS CEREBERUS (ARIZONA BLACK RATTLESNAKE).
EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; REPTILIA;
 Score 249; DB 1; Length 72;
Pred. No. 1.61e-38;
11; Mismatches 22; Indels
 72 AA
 PRT;
 PRT;
 SPECIES-T.ALBOLABRIS; TISSUE-VENOM;
 SPECIES-T.GRAMINEUS; TISSUE-VENOM;
 Query Match
Best Local Similarity 46.8%;
Matches 29; Conservative
 STANDARD;
 STANDARD;
 MEDLINE; 90207217
 TISSUE-VENOM;
 LT 6
DISI_CROVE
P31985;
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 DISG_TRIGA
P17496;
 RF 71
 62
 62
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 SEQUENCE
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 MEDLINE; 9312315.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-! FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SUBRACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 INHIBLY AND COLLEGEN.
-!- SIMILARIY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; 643019; 643019.
PIR; 643019; 743019.
PIR; 643019; PIR 643019.
SITE PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SITE S50 52 CELL ADHESION; VENOM.
SITE 71 AA: 7637 MW; 910AF02C CRC32;
 JECH; 31-CCI->>.
IECH; SACO427; DISINTEGRINS; 1.
COAGULATION; PLATELET; CELL ADHESION; VENOM; 3D-STRUCTURE.
COAGULATION; PARROLIDONE CARBOXYLIC ACID (IN ALPHA-2
 9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68
 Gaps
 0; Gaps
 -i- THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
-i- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-ILIA PROTEIN
-i- MTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR: A32029; A32082.
PIR: A35982; A35982.
PIR: S29198; S29198.
PIR: S29198; S29198.
 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
CROTALUS VIRIDIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
EUKARYOTA: METALOS. CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
 Score 250; DB 1; Length 71;
Pred. No. 9.24e-39;
11; Mismatches 22; Indels
 Length 49;
 5; Mismatches 11; Indels
 CELL ATTACHMENT SITE.
MISSING (IN ALPHA-2 FORM).
 1 QCESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKG 46
 Score 253; DB 1;
Pred. No. 1.74e-39;
 OA851E33 CRC32;
 71 AA.
 PROBABLE.
 PROBABLE.
 PRT;
 01-JUL-1993 (REL. 26, CREATED)
 5424 MW;
 49.8%;
llarity 65.2%;
Conservative
 49.2%;
Similarity 46.8%;
29; Conservative
 STANDARD;
 Local Similarity
 Query Match
Best Local Similarity
 TISSUE-VENOM;
 30:
 DISI_CROVV
P31987;
 STRAND
 DISULFID
 [1]
SEQUENCE.
 DISULFID
 DISULFID
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 VARIANT
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Matches

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Gaps

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01-A0G-1990 (REL. 15, CREATED)
01-A0G-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DISINTERIN TRIGRAMIN GAMMA (ALBOLABRIN) (PLATELET AGGREGATION
ACTIVATION INHIBITOR).
TRIMBERSUNGS GRAMINGUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE),
AND TRIMBERSUNGS ALBOLABRIS (WHITE-LIPPED PIT VIPER).
LEPIDOSAURIA; SERPENTES.
 DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A., DEISHER T.A., BUNTING S., LAZARUS R.A.; PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
 MEDLINE; 90283463.
WILLIAMS J., RUCINSKI B., HOLT J., NIEWIAROWSKI S.;
73 AA
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Best Loca Matches

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FACTOR AND COLLAGEN
 9
DISI_BOTAT
P18618;
 DISI_BOTCO
P31988;
 SEQUENCE
 Query Match
 Matches
 Best
 RESULT
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 HANG OCCUPATION RANGE OCCUPATION
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 MEDLINE, 97052455.

SMITH K.J. JASEJA M., LU X., WILLIAMS J.A., HYDE E.I., TRAYER I.P.;
INT. J. PEPT. PROTAIN RES. 48:220-228(1996).

-!- FUNCTION: INHIBITS FIBRINGGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIS LIBA COMPLEX. ACT BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SUFRACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 SOSZKA T., LU W., COOK J.J., JAMESON B.A.,
 SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN 69
 JASEJA M., SMITH K.J., LU X., WILLIAMS J.A., TRAYER H., TRAYER I.P., HYDE E.I.;
 Gaps
 -!- SIMILARITY:
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR; E35982; E35982.
PIR; A23731; A23731.
PIR; 543021; $43021.
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN MOLOSSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS MOLOSSUS MOLOSSUS (NORTHERN BLACK-TAILED RATLESNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 ö
 Score 248; DB 1; Length 73;
Pred. No. 2.81e-38;
9; Mismatches 22; Indels
 CELL ATTACHMENT SITE. DA64D759 CRC32;
 ; DISINTEGRINS; 1.
N; PLATELET; CELL ADHESION; VENOM.
15 PROBABLE.
 73 AA.
BIOCHIM. BIOPHYS. ACTA 1039:81-89(1990).
 PROBABLE
 PROBABLE
 PROBABLE
 J. BIOCHEM. 218:853-860(1993).
 PRT;
 SPECIES-T. ALBOLABRIS;
MEDLINE; 91242430.
CALVETE J.J., SCHAEFER W., SOSZK
NIEMTAROWSKI S.;
BIOCHEMISTRY 30:5225-5229(1991).
 BLOOD COAGULATION; PLATELET;
 7573 MW;
 Query Match 48.8%;
Best Local Similarity 48.3%;
Matches 29; Conservative
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 SPECIES-T.ALBOLABRIS;
MEDLINE; 94109384.
 SPECIES-T.ALBOLABRIS;
 HSSP; P17494; 1KST
PROSITE; PS00427; 1
 AA;
 MEDLINE; 97052455
 AND COLLAGEN.
 [5]
STRUCTURE BY NMR
 DISULFIDE BONDS
 STRUCTURE BY
 TISSUE=VENOM;
 DISI_CROMM
P31984;
 DISULFID
DISULFID
 DISULFID
 SEOUENCE
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01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-UUJ-1993 (REL. 26, LAST ANNORATION UPDATE)
01-UUJ-1993 (REL. 26, LAST ANNORATION UPDATE)
DISINTEGRIN BATROXOSTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS ATROX (BARBA AMARILLA) (FER-DE-LANCE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
BIRS, H43019; H43019; H8ST.
PROSITE; PSO0477; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
51
SITE
51
SHOW, 7312E08D CRC32;
 Gaps
 Gaps
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 13 NPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNRF 71
 13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANORATION UPDATE)
DISINTEGRIN COTIARIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
 BOTHROPS COTIARA (COTIARA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
 ö
 TISSUE=VENOM;
MEDLINE; 93123215.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
 Length 73;
 Length 71;
 22; Indels
 21; Indels
 Score 248; DB 1;
Pred. No. 2.81e-38;
9; Mismatches 21
 Score 246; DB 1;
Pred. No. 8.53e-38;
 7; Mismatches
 71 AA.
 72 AA
 PRT;
 PRT;
 48.4%;
 Ouery Match
Best Local Similarity 49.2%;
 30; Conservative
 STANDARD:
 STANDARD;
 Local Similarity
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Matches

셤 ô

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HUANG T.-F., HOLT J.C., LUKASIEWICZ H., NIEWIAROWSKI S.;

L J. BIOL. CHEM. 262:16157-16163(1987).

- I- FUNCTION: THES PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT ACTS IN HEMORRHAGE (EN SIMILARITY).

- I- FUNCTION: TRIGRAMIN INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBITS AGREGATION UNDUCED BY ADP, THROMBIN,

- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY.

- TORACTOR: BLOMGS TO PEPTIDASE FAMILY MI2B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY REGION, TO OTHER DISINTEGRINS.
 INNLBITOK)).
TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).
EUGRARYOTR: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 PUTATIVE VENOM METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) (CONTAINS: DISINTEGRIN TRIGRAMIN ALPHA (PLATELET AGGREGATION ACTIVATION
 R.M., LIPARI M.T., NAPIER M.A., IS R.A.;
 PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
HYDROLASE; METALLOPROTEASE; ZINC; BLOOD COAGULATION; PLATELET;
CELL ADHESION; VENOM; ZYMOGEN, SIGNAL.
SIGNAL
 PUTATIVE ZINC METALLOPROTEINASE. TRIGRAMIN.
 ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
 Length 480;
 Score 245; DB 1; Length 480
Pred. No. 1.49e-37;
11; Mismatches 24; Indels
 KIRBY E.P., NIEWIAROWSKI
 MEDLINE; 90207217.
DENNIS M.S., HENREL W.J., PITTI R.M., LIPARI M.T
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990)
 D59DA91F CRC32;
 POTENTIAL.
 SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
MEDLINE; 90332429,
MEDER M.P., JACOBSON M.A.;
NUCLEIC ACIDS RES. 18:4255-4255(1990).
 HUANG T.-F., HOLT J.C., KIRBY 1
BIOCHEMISTRY 28:661-666(1989).
 53494 MW;
 Query Match 48.2%;
Best Local Similarity 43.5%;
Matches 27; Conservative
 4445
4442
4466
4473
279
 407
 EMBL; X51530; G64408;
 SEQUENCE OF 408-419.
 SEQUENCE OF 408-479.
 SEQUENCE OF 408-479.
 PIR; A29784; A29784
PIR; A30065; A30065
 454
458
279
480 AA;
 89229063
 88058981
 PIR; A30065; A
HSSP; P34179;
 IISSUE "VENOM;
 MEDLINE;
HUANG I.-
 METAL
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 MEDLINE;
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 SEQUENCE
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MEDLINE; 9312315.
SCARBOKOGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.,
J. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
 -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
HSSP, A43020.
HSSP; P14494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 66 BY SIMILARITY.
SITE 51 53 CELL ATTACHHENT SITE (POTENTIAL).
SEQUENCE 73 AA; 7739 MW; 15EEAA7A CRC32;
 Gaps
 Gaps
 13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
 + HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRY 62
 13 NPCCDAATCKLRPGAQCAEGLCCDQCRFKGAGKICRRARGDNPDDRCTGQSADCPRNRF 71
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN JARARACIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS JARARACA (JARARACA).
EUKARXOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 CELL ATTACHMENT SITE (POTENTIAL). 0D73D088 CRC32;
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 ö
 Score 246; DB 1; Length 73;
Pred. No. 8.53e-38;
7; Mismatches 22; Indels
 Score 246; DB 1; Length 72;
Pred. No. 8.53e-38;
7; Mismatches 22; Indels
 BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULFID 47 66 BY SIMILARITY.
 (REL. 14, CREATED)
(REL. 23, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
 480 AA
 73 AA
 PRT;
 PRT;
 72 AA; 7709 MW;
 48.48;
 48.4%;
50.8%;
 Conservative
 30; Conservative
 STANDARD;
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 Local Similarity
 Local Similarity
 LT 12
DISA_TRIGA
P15503;
01-APR-1990
01-AUG-1992
01-NOV-1995
 TISSUE-VENOM;
 LT 11
DISI_BOTJA
P31989;
 Query Match
Best Local S
 SEQUENCE
 SEQUENCE
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Gaps

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Best Loca Matches

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PIR; A43296;
 LT 15
HRTE_CROAT
 71 Y 71
 62 Y 62
 ACT_SITE
METAL
 Query Match
 DISULFID
 PROPEP
 CHAIN
 CHAIN
 METAL
 Matches
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 HE THE THE TENDERS OF COCCOCCO STANK SERVICE ö
 TISSUE-VENOM;
MEDLINE; 93123215.
MEDLINE; 93123215.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-! FUNCTION: INHIBITES FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROFEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
417 SPANPCCDAATCKLIPGAQCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCNGRSAGCPRN 476
 FACTOR AND COLLAGEN.
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; 143019: 143019.
 SPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN BASILICIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS BASILICUS (MEXICAN WEST-COAST RATLESNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISJUTEGRIN LACHESIN (PLAFELET AGGREGATION ACTIVATION INHIBITOR)
 LACHESIS MUTA MUTA (BUSHMASTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 HSSP; P1484; 1851.
PROSITE; PS00427; DISINTEGRINS; 1.
PLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
52 CELL ATTACHMENT SITE (POTENTIAL).
FANTACHMENT 72 AA: 7704 MW; 4B255615 CRC32;
 ö
 Length 72;
 22; Indels
 Score 242; DB 1; 1
Pred. No. 7.84e-37;
 12; Mismatches
 73 AA.
 72 AA
 PRT;
 PRT;
 47.6%;
larity 45.2%;
Conservative
 STANDARD;
 STANDARD;
 LEPIDOSAURIA; SERPENTES.
 Query Match
Best Local Similarity
28; Conserv
 HSSP; P17494; 1KST
 TISSUE-VENOM;
 PF 478
 DISI_LACMU
P31990;
 62
 DISI_CROBA
 HF 70
 62
 SEQUENCE
 SEQUENCE
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CHILDRICAL STRONG THIS PROTEIN LIBER OF THE PROTEGE FROM SNAKE VENOM THAT ACTS IN HEMORRHAGE.

-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROPEIN ITB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROPEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT AND COLLAGEN (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: CLEAVAGE OF 3-ASN-|-GLN-4, 9-SER-|-HIS-10 AND 14-ALA-LEU-15 BONDS IN INSULIN B CHAIN AND 14-TYR-|-GLNI-5 AND CHAIN. CLEAVASE TYPE IV COLLAGEN AT 258-ARA-|-CLNI-259 IN ALPHA-1-(IV) AND AT 191-GLY-|-LEU-192 IN ALPHA-2-(IV).

-!- COPACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY:

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MISB (ZINC METALLOPROTERSES): ALSO KNOWN AS THE REPROLESIN SUBFAMILY.

-!- SIMILARITY: HELONGS IN THE MIDDLE REGION, TO DISINTEGRINS.
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INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 -!- STMILARITY: CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
B13019; E43019.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 51 CELL ATTACHENT SITE (POTENTIAL).
SEQUENCE 73 AA; 7765 MW; 08C5DFBO CRC32;
 11 PANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNG 70
 SVHPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNR 61
 Gaps
 HEMORRHAGIC METALLOPROTEINASE HT-E. DISINTEGRIN (POTENTIAL).
 PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00427; DISIMPEGRINS; 1.
HYDROLASE; WETALLOPROTEASE; ZINC; BLOOD COAGULATION; PLATELET;
CELL ADHESION; VENOM; ZYMOGEN; SIGNAL.
SIGNAL
 01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-ROY-1995 (REL. 32, LAST ANNOTATION UPDATE)
HEMORRHAGIC METALLOPROTEINASE HT-E PRECURSOR (EC 3.4.24.44)
(ATROLYSIN B) (HEMORRHAGIC TOXIN B).
CROYALUS ATROX (WESTERN DIAMONDBACK RATILESNAKE).
EUKARYOTA: METAZOA, CHORDATA, VERTEBRATA; TETRAPODA; REPITLIA,
 ö
 ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
SINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
 Length 73;
 Indels
 HITE L.A., SHANNON J.D., BJARNASON J.B., FOX J.W., BIOCHEMISTRY 31:6203-6211(1992).
 23;
 Score 239; DB 1;
Pred. No. 4.12e-36;
9; Mismatches 23
 478 AA
 POTENTIAL
 PRT;
 47.08;
 Conservative
 EMBL; M89784; G213030; -. PIR; A43296; A43296.
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 FACTOR AND COLLAGEN
 187
389
339
333
339
 Local Similarity
les 29; Conser
 SEQUENCE FROM N.A.
 MEDLINE; 92329442.
 HSSP; P34179;
PROSITE; PS001
 TISSUE-VENOM;
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FT DISULFID 344 351 BY SIMILARITY.
SO SEQUENCE 478 AA; 53637 MW; E92A2DA7 CRC32;
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0; Gaps Ouery Match 46.7%; Score 237; DB 1; Length 478; Best Local Similarity 47.4%; Pred. No. 1.25e-35; Matches 27; Conservative 11; Mismatches 19; Indels

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Search completed: Fri Sep 25 13:18:34 1998 Job time : 6 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Sep 25 13:19:27 1998; MasPar time 5.61 Seconds 436.536 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>PCT-US98-16719-20 (1-67) from PCTUS9816719A.pep 508 1 NSVHPCCDPVXCEPREGEHC......DYCTGISXDCPRNRYKGKED 67 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 32.783; Variance 59.804; scale 0.548 Statistics:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Pred. No.                | 1.49e-62              | 4.42e-36              | 1.30e-34 | 3.42e-34 | 5.53e-34             | 2.34e-33             | 3.79e-33              | 3.79e-33             | 3.79e-33             | 6.13e-33              | 6.13e-33              | 6.13e-33             | 1.60e-32              | 1.60e-32             | 1.60e-32             | 2.58e-32              | 1.09e-31             | 4.57e-31             | 1.19e-30              | 1.91e-30              | 2.07e-29 | 2.07e-29             | 5.35e-29             |
|-----------|--------------------------|-----------------------|-----------------------|----------|----------|----------------------|----------------------|-----------------------|----------------------|----------------------|-----------------------|-----------------------|----------------------|-----------------------|----------------------|----------------------|-----------------------|----------------------|----------------------|-----------------------|-----------------------|----------|----------------------|----------------------|
|           | Description              | fibrinolytic metallop | applaggin - eastern c | ğ        | 03       | echistatin alpha-2 - | platelet aggregation | echistatin (NMR, 8 st | echistatin alpha-1 - | platelet aggregation | albolabrin - green pi | trigramin gamma - Ind | platelet aggregation | batroxostatin - barba | platelet aggregation | platelet aggregation | trigramin precursor - | platelet aggregation | platelet aggregation | atrolysin E (EC 3.4.2 | echistatin gamma - sa | á        | platelet aggregation | platelet aggregation |
| SUMMAKIES | ΙD                       | JC4880                | A33990                | D35982   | S53431   | A35982               | G43019               | 2ECH                  | A32029               | B43020               | A23731                | E35982                | H43019               | S13168                | F43019               | A43020               | A30065                | I43019               | E43019               | A43296                | S53432                | A40003   | B40003               | B43019               |
|           | 80                       | ~                     | ~                     | ~        | 7        | ~                    | N                    | S                     | ~                    | ~                    | ~                     | 7                     | ~                    | 7                     | ~                    | 7                    | Н                     | ~                    | ~                    | 7                     | ~                     | ~        | N                    | ~                    |
|           | Query<br>Match Length DB | 478                   | 71                    | 73       | 20       | 47                   | 71                   | 49                    | 49                   | 72                   | 73                    | 73                    | 73                   | 71                    | 72                   | 73                   | 480                   | 72                   | 73                   | 478                   | 49                    | 73       | 73                   | 72                   |
| æ         | Query<br>Match           | 76.0                  | 51.8                  | 50.4     | 50.0     | 49.8                 | 49.5                 | 49.0                  | 49.0                 | 49.0                 | 48.8                  | 48.8                  | 48.8                 | 48.4                  | 48.4                 | 48.4                 | 48.2                  | 47.6                 | 47.0                 | 46.7                  | 46.5                  | 45.5     | 45.5                 | 45.1                 |
|           | Score                    | 386                   | 263                   | 256      | 254      | 253                  | 250                  | 249                   | 249                  | 249                  | 248                   | 248                   | 248                  | 246                   | 246                  | 246                  | 245                   | 242                  | 239                  | 237                   | 236                   | 231      | 231                  | 229                  |
|           | Result<br>No.            | н                     | 7                     | m        | 4        | S                    | ø                    | 7                     | ω                    | σ                    | 10                    | 11                    | 12                   | 13                    | 14                   | 15                   | 16                    | 17                   | 18                   | 19                    | 20                    | 21       | 22                   | 23                   |

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Gaps

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Score 386; DB 2; Length 478; Pred. No. 1.49e-62; 7; Mismatches 10; Indels

Query Match
Best Local Similarity 73.0%;
Matches 46; Conservative

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415 NSGNPCCDPVTCQPRRGEHCVSGKCCRNCKFLRAGTVCKRAVGDDMDYCTGISSDCPRN 474

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Gaps

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saw-scaled viper

ACCESSIONS

ORGANISM

DATE

RESULT

REFERENCE

475

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Chen, Y.L.; Huang, T.F.; Chen, S.W.; Tsai, I.H.
Biochem. J. (1995) 305:513-520
Determination of the structure of two novel echistatin
variants and comparison of the ability of echistatin
variants to inhibit aggregation of platelets from different
 A35982 #type complete
echistatin alpha-2 - saw scaled viper
echistatin alpha-2 - saw scaled viper
#formal_name Echis carinatus #common_name saw-scaled viper
09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
05-Dec-1997
 #superfamily unassigned disintegrins; disintegrin homology
 Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.;
Napier, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein Ilb-IIIa protein antagonists from sr
venoms: evidence for a family of platelet-aggregation
 10 SPANPCCDAATCKLLPGAQCGEGPCCDQCSFMKKGTICRRARGDDLDDYCNGRSAGCPRN 69
 echistatin beta - saw-scaled viper
#formal_name Echis carinatus #common_name saw-scaled vip
01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change
21-Nov-1997
$53431
 (fragment) #label
 *superfamily unassigned disintegrins; disintegrin |
#length 47 #molecular-weight 5252 #checksum 3850
 #checksum 4266
 Length 50;
 Score 253; DB 2; Length 47;
Pred. No. 5.53e-34;
5; Mismatches 11; Indels
 CASGPCCRDCKFLKEGTICKRARGDNMDDYCNGKTCDCPRNPHKGEHD 49
 1 QCESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKG 46
 20 CISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNRYKGKED
 Score 254; DB 2; I
Pred. No. 3.42e-34;
5; Mismatches 13;
 #domain disintegrin homology (
#length 50 #molecular-weight 5562
 #type complete
 ##molecule_type protein
##residues 1-50 ##label CHE
 1-47 ##label DEN
 10;
 #cross-references MUID:90207217
 preliminary
 preliminary
 50.0%;
larity 62.5%;
Conservative
 Query Match
Best Local Similarity 65.2%;
Matches 30; Conservative
 ##molecule_type protein
 inhibitors
 species.
S53431
 Local Similarity
es 30; Conser
 A35982
 A35982
 29;
 ##residues
 62
 70 PF 71
 CLASSIFICATION
SUMMARY
 CLASSIFICATION
 ##status
 ##status
 Query Match
Best Local S
 RY
 #accession
 #accession
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 #authors
 #authors
 ACCESSIONS
REFERENCE
 #journal
#title
 #journal
 ACCESSIONS
 61
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 Matches
 Matches
 REFERENCE
 #title
 ORGANISM
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 RESULT
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 Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.;
Npier, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence for a family of platelet-aggregation
 #authors Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marzec,
U.M.; Harker, L.A.; Maraganore, J.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8050-8054
#title Agkistrodon piscivorus piscivorus platelet aggregation
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 Pelton, J.T.; Atkinson, R.A.; Saudek, V.
submitted to the Brookhaven Protein Data Bank, April 1993
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 9 SPANPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 68
 Saudek, V.; Atkinson, R.A.; Pelton, J.T.
Blochemistry (1991) 30:7369
Three-dimensional structure of echistatin, the smallest active rad protein.
Resolution: not applicable
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12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
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J. Biol. Chem. (1993) 268:1058-1065
Characterization of the integrin specificities of
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 Saudek, V.; Atkinson, R.A.; Lepage, P.; Pelton, J.T.
Eur. J. Biochem. (1991) 202:329
The secondary structure of echistatin from 1h-NMR,
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12 Mar-1993 #sequence_revision 12-Mar-1993 #text_change
 #authors Gan, Z.R.; Gould, R.J.; Jacobs, J.W.; Friedman, P.A.;
Polokoff, M.A.
#journal J. Biol. Cana. (1988) 263:19827-19832
#title Echistatin. A potent platelet aggregation inhibitor from the venom of the viper, Echis carinatus.
#cross-references MUID:89066819
#accession A32029
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 #authors Calvete, J.J.; Wang, Y.; Mann, K.; Schaefer, W.;
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#journal FEBS Lett. (1992) 309:316-320
#title The disulfide bridge pattern of snake venom disintegrins,
flavoridin and echistatin.
 Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, A.; Campbell, A.M.; Charo,
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Characterization of the integrin specificities of
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 2 CESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKG 46
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09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
 Jaseja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.I.

Fur. J. Blochem. (1993) 218:853-860
(1.1H-NMR studies and secondary structure of the RGP-containing snake toxin, albolabrin.
 ö
 Calvete, J.J.; Schaefer, W.; Soszka, T.; Lu, W.; Cook, J.J.;
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 #journal Biochemistry (1991) 30:52525-5229
#title Identification of the disulfide bond pattern in albolabrin, an RGD-containing peptide from the venom of Trimeresurus albolabris: significance for the expression of platelet aggregation inhibitory activity.
 inhibits cell adhesion and platelet aggregation *superfamily unassigned disintegrins; disintegrin homology venom
 Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.;
Napier, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A.
 10 SPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN 69
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Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein IID-IIIa protein antagonists from snake venoms: evidence for a family of platelet-aggregation inhibitors.
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12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
29-Aug-1997
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 10 SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN 69
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 #authors Rucinski, B.; Niewiarowski, S.; Holt, J.C.; Soszka, T.; Rndsen, K.A.
#journal Biochim. Biophys. Acta (1990) 1054:257-262
#title Batroxostettin, an Arg-Gly-Asp-containing peptide from Bothrops atrox, is a potent inhibitor of platelet aggregation and cell interaction with fibronectin.
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 13 NPCCDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRNRF 71
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Characterization of the integrin specificities of
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm APsrch\_pp

MasPar time 6.57 Seconds 429.673 Million cell updates/sec Fri Sep 25 13:23:33 1998; Run on:

Tabular output not generated.

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TABLE unitprotable Gap 60 Scoring table:

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Minimum Match 0% Listing first 45 summaries Post-processing:

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Mean 2.792; Variance 0.403; scale 6.929 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| m             | Ø     | 9.4            | 169       | σ  | 028458 | TRANSCRIPTIONAL REGULA | 6.08e+00  |
| 4             | 9     | 9.4            | 198       | 7  | 986600 | LACTOBACILLUS BACTERIO | 6.08e+00  |
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| ø             | 9     | 9.4            | 257       | 11 | 068385 |                        | 6.08e+00  |
| 7             | ø     | 9.4            | 272       | 0  | 033292 | DEHYDROGENASE,         | 6.08e+00  |
| <b>&amp;</b>  | 9     | 4.             | 453       | σ  | P72834 | UDP-GLUCOSE DEHYDROGEN | 6.08e+00  |
| 0             | 9     | 4.6            | 453       | Н  | 005979 | SIMILARITY TO KYNURENI | 6.08e+00  |
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| 11            | φ     | 9.4            | 481       | 12 | 091505 | PRO-TRIMUCIN PRECURSOR | 6.08e+00  |
| 12            | 9     | 9.4            | 487       | 12 | 092119 | ATROLYSIN E PRECURSOR  | 6.08e+00  |
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| 1.T 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                          | CREAT<br>LAST<br>LAST                         | NTINE VIPE<br>SUKARYOTES<br>JEROGLOSSA<br>OVIPERA.                   | A.T., SIIGUR<br>UN. 224:229-3<br>XINS; 1.<br>PLATELET; CEI<br>POTENTIAL.<br>POTENTIAL.<br>M; 384418C4                                                                       | ×                                                                           |                           |
| U.T. 1 098995 01-FEB-199 01-FEB-199 01-TEB-199 01-JAN-199 01-JAN-199 01-JAN-199 01-SBN-199 01-JAN-199 01-SBN-199 01-SBN-199 01-SBN-199 01-SBN-199 01-NOV-1999 01-NOV-1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PRELIMINARY              | (TREMBLREL.<br>(TREMBLREL.<br>(TREMBLREL.     | A LEBETINA (LEVAL); MITOCHONDRIAL 11A; SQUAMATA; SCI VIPERINAE; MACK | NOM N.A.  DM GLAND;  AASPOLLU A., TU  10PHYS. RES. COM  94; E246059;  S00427; DISINTEGI  OOD COAGULATION;  1 18  194  478  A78  A78  A78  A88                               | > 4 0                                                                       | PRELIMIN?                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | LT 1<br>098995<br>098995 | 01-FEB-1997<br>01-FEB-1997<br>01-JAN-1998     | MACROVIPER,<br>EUKARYOTAE,<br>LEPIDOSAUR;<br>VIPERIDAE;              | SEQUENCE FI<br>TISSUE-VEN<br>SIGURE,<br>BICCHEM, BI<br>EMBL; X9789<br>SIGNAL; BLC<br>SIGNAL; BLC<br>SIGNAL; BLC<br>SIGNAL; BLC<br>SIGNAL; BLC<br>SIGNAL; BLC<br>SIGNAL; BLC | ery Match st Local Sin tches 12; 462 DYCTG1                                 | LT 2<br>Q90222<br>Q90222; |

KAKIKAWA M., WATANABE N., HIRAKAWA M.,

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MEDLINE; 97225795.

KODAIRA K.I., OKI M., KI YAMADA K., TAKETO A.;
GENE 187:45-53(1997).

EMBL; X98106; E247161;
RORF198.
BACTERIOPHAGE PHIGIE.
VIRUSES.
 SEQUENCE FROM N.A.
 28 NCKFLN
 SEQUENCE
 SEQUENCE
 LT 6
Q68385
Q68385;
 л 5
029216
029216;
 Matches
 Matches
 RESULT
 RESULT
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 SO SERVER BENEVIA
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 KLENK H.P., CLATYON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRRIDES N.C., FLEISCHAANN R.D., OUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., OUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., COUACKENBUSH J., MCNENLE K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK GOCAYNE J.D., WELDMAN J.F., MCNONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJIT C., GARLAND S.A., MASON T.M., CLSEN G.J., FRASER C.M., SHITH H.O., WOESE C.R., VEYTER J.C.; SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRRIDES N.C., FLEISCHHANN R.D., OUACKENBUSH J., LEE N.H., SULTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEX K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R., SACANE J.D., WEIDMAN J.F., MCNONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KALNE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJI C., GARLAND S.A., MASON T.M., OLSN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

ENBL: AEO00977; G2648728; SEQUENCE 169 AA: 19917 MW; BOEC6237 CRC32;
 Gaps
 Gaps
 ARCHAEOGLOBUS FULGIDUS.
ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
 FUJISAMA Y., KURODA S.I., NOTOXA K., KONISHI H., TERASHITA Z.I.; TAKEDA KENKYUSHO HO 53:39-56(1994).

EMBL: D28871; G559299; -.

PROSITE; PS00427; DISINTEGRINS; 1.

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

NON_TER 1 1

SEQUENCE 115 AA; 12389 MW; C10C6FAF CRC32;
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 ö
 Ouery Match 9.4%; Score 6; DB 9; Length 169; Best Local Similarity 100.0%; Pred. No. 6.08e+00; Matches 6; Conservative 0; Mismatches 0; Indels
 DB 12; Length 115; 6.08e+00;
 1; Indels
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANOTATION UPDATE)
PHIGLE COMPLETE GENOMIC DNA.
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATORY PROTEIN, TETR PAMILY.
 0; Mismatches
 198 AA
 169 AA.
 Score 6;
Pred. No.
 PRT;
 PRT;
 ULT 4 PRELIMINARY;
003936;
01-301-1997 (TREMBLREL. 04, CR
01-JUL-1997 (TREMBLREL. 05, LA
01-JAN-1998 (TREMBLREL. 05, LA
LACTOBACILLUS BACTERIOPHAGE PH
 PRELIMINARY;
 Query Match 9.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
 SEQUENCE FROM N.A.
 107 SADCPRN 113
 I IIIII
SXDCPRN 60
 134 AMLDGL 139
 41 AMLDGL 46
 TISSUE-LIVER;
 LT 3
028458
028458;
 54
 RESULT
 RESULT
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 KLENK H.P., CLATTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A., DODSON N.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL I.K., BADGER J.H., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN J.F., MCNOBALD I., QUARRAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; SUBMITTED (NOV-1997) TO EMBLYGENBANK D.DBA DATA BANKS.
 KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A., DODSON N.J., GRAINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHHANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU I., OVERBEEK R., GOCANNE J.D., WEIDMAN J.F., MCNONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., DOWANN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 Gaps
 Gaps
 ARCHAEOGLOBUS FULGIDUS.
ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE
 ö
 ö
 0; Indels
 Length 223;
 0; Indels
 Length 198;
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
HYPOTHETICAL 25.9 KD PROTEIN.
 DB 9; Ler
6.08e+00;
 DB 7; Ler
6.08e+00;
 223 AA; 25874 MW; 0042F3FF CRC32;
198 AA; 22540 MW; CA722A39 CRC32;
 Ā
 Score 6; DB 9;
Pred. No. 6.08e+
0; Mismatches
 Score 6; DB 7;
Pred. No. 6.08e+
0; Mismatches
 257
 PRT;
 PRELIMINARY; PRT;
 PRELIMINARY;
 Query Match
Best Local Similarity 100.08;
 Query Match 9.4%;
Best Local Similarity 100.0%;
 Conservative
 6; Conservative
 HYPOTHETICAL PROTEIN
 138 AMLDGL 143
 33
 69 NCKFLN 74
 41 AMLDGL 46
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Gaps

S.

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STRAIN-PCC6803;
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATEUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKDWURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
 2.,
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 SEQUENCE FROM N.A.

STRAIN-S28GC (AA972);
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU :
FOATELO M., FULFON L., GATTUNG S., GRECO T., KIRSTEN J.,
KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T.,
MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUSO I
RIEKEL L., TAICH A., TREVASKIS E., VIGNATI D.,
WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.,
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 0; Indels
 0; Indels
 Score 6; DB 9; Length 453; Pred. No. 6.08e+00;
 Score 6; DB 1; Length 453;
Pred. No. 6.08e+00;
0; Mismatches 0; Indels
 SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
WATERSTON R.;
WATERSTON R.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U19027; G609377; -.
SEQUENCE 453 AA; 51032 MW; F015FAB2 CRC32;
 TO EMBL/GENBANK/DDBJ DATA BANKS
 SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 L8083.14.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 DNA RES. 3:109-136(1996).
EMBL; D90901; G1651923; -.
SEQUENCE 453 Aa; 49097 MW; CC5B4A7D CRC32;
 Š
 0; Mismatches
 453 AA.
 RESULT 10

ID Q18026 PRELIMINARY; PRT;

AC 018026;

DT 01-NOV-1996 (TREMBLREL, 01, CREATED)
 PRT;
 01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
 PRELIMINARY;
 / Match 100.0%; Local Similarity 100.0%; nes 6; Conservative
 / Match 9.4%;
Local Similarity 100.0%;
nes 6; Conservative
 SIMILARITY TO KYNURENINASE.
 SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
HALLSWORTH K.;
 SUBMITTED (JUN-1996)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 270 KFLNAG 275
 STRAIN-PCC6803;
 166 EPREGE 171
 30 KFLNAG 35
 |||||||
EPREGE 18
 TABATA S
 Query Match
 Query Match
 7T 9
 005979;
 13
 Matches
 RESULT
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 STRAIN-TOLEDO;
MEDLINE; 96099416.
CHA T.A., TOM E., KEMBLE G.W., DUKE G.M., MOCARSKI E.S., SPAETE R.R.;
J. VIROL. 70:78-83(1996).
EMBL; U33331; G1167918; -
SEQUENCE 257 AA; 27471 MW; EC259DCB CRC32;
 Gaps
 VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE
 Gaps
 STRAIN=H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 ö
 ö
 PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
 0; Indels
 0; Indels
 DB 11; Length 257
6.08e+00;
 P72834
P72834
P72834:

 Score 6; DB 9; Length 272;
Pred. No. 6.08e+00;
0; Mismatches 0; Indels
 STRAIN-H37RV;
MURPHY L., HARRIS D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 STRAIN-H37RV;
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; ALO08967; E1173880; -.
SEQUENCE 272 AA; 28223 MW; 11FBAOFD CRC32;
 0; Mismatches
 272 AA
 Score 6; 1
Pred. No. (
 CREATED)
 PRT;
 05,
05,
 PRELIMINARY;
 Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match 9.4%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 MYCOBACTERIUM TUBERCULOSIS.
 01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
 01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
 01-NOV-1996 (TREMBLREL.
 HUMAN CYTOMEGALOVIRUS
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 97 CISGPC 102
 196 NSVHPC 201
 111111
20 CISGPC 25
 1 NSVHPC 6
 DEHYDROGENASE
 ORF UL133.
 COLE S.T
 LT 7
033292
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RESULT ID 03

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Gaps

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9.4%;
larity 85.7%;
Conservative
 05,
05,
 PRELIMINARY;
 PRELIMINARY;
 11 13 PRELIMINA 034722 O34722; 01-JAN-1998 (TREMBLREL.
 01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
 SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
MEDLINE; 96067555.
 487 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 477 SADCPRN 483
 54 SXDCPRN 60
 54 SXDCPRN 60
 YFMG PROTEIN.
 Q92119;
01-NOV-1996
 9
 STRAIN-168;
 SEQUENCE
 Query Match
 T 12
092119
 SIGNAL
 Matches
 RESULT
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 A MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
A BONTELLD J., BURTON J., CONNELL M., COSEY T.,
COLLSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
JOHNSTON L., GARDNER A., GERSEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., ILSTER N.,
LATREILLE P., LIGHTHING J., LLOYD C., MCMURRAY A., MCRIMORE B.,
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
SAUNDERS D., SHOWNKEN R., SMALDON N., SMITH A., SONNHAMMER E.,
A STADER R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
MILKINSON SPROAT J., WOHLDMAN P.;
MATURE 368:32-38(1994).
 SECUENCE FROM N.A.
TISSUB-SONARE VENOM GLAND;
TISSUB-SONARE VENOM GLAND;
TISSUB-SONARE VENOM
TISSUB-SONARE VENOM
TOTAL J.H., WANG Y.M., LAER Y.H.;
BIOCHIM. BIOPHYS. ACTA 1200:337-340(1994).
EMBL: X77089; G467704; -
EMBL: X77089; G467704; -
EMBL: PSOSATE: PSOSATE SECRIVE; 1
SIGNAL; METALLOPROTEASE: BLOOD COAGULATION; PLATELET; CELL ADHESION;
 Gaps
 Gaps
 EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 PRO-TRIMUCIN PRECURSOR.
TRIMBRESURUS MUCROSOURAMIUS (TAIWAN HABU).
EUKARYOTA. METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
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 Score 6; DB 12; Length 481;
Pred. No. 6.08e+00;
 1; Indels
 0; Indels
 Length 478;
 STRAIN-BRISTOL N2;
BENTLEY D.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
 TO EMBL/GENBANK/DDBJ DATA BANKS
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
 Score 6; DB 3; Le
Pred. No. 6.08e+00;
0; Mismatches 0
 481 PRO-TRIMUCIN.
54079 MW; 23A332F0 CRC32;
 STRAIN-BRISTOL N2;
WATERSTON R.;
SUBMITTED (APP-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; U56965; G1293837; -.
SEQUENCE 478 Aa; 54049 MW; 274B0462 CRC32;
 0; Mismatches
 481 AA.
 POTENTIAL
 01-NOV-1996 (TREMBLREL. 01, LAST ANNO)
SIMILAR TO R. NORVEGICUS KYNURENINASE.
 PRT;
 PRELIMINARY;
 9.48;
 Best Local Similarity 85.7%;
Matches 6; Conservative
 Ouery Match 9.4%;
Best Local Similarity 100.0%;
 6; Conservative
 01-NOV-1996 (TREMBLREL.
 CAENORHABDITIS ELEGANS
 481 AA;
 STRAIN-BRISTOL N2;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 471 SADCPRN 477
 204 EPREGE 209
 13 EPREGE 18
 SEQUENCE
 Query Match
 LT 11
Q91505
Q91505;
 SIGNAL
 VENOM
 Matches
 RESULT
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 KUNSTE'L, OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
KA ZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER I., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
BROUILLET S., BRUGSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
A GHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BENIZOT F., DEVINE K.M., DUSTERHOFT A., ERRILCH S.D., EMMERSON P.T.,
A ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
A GHIM S.Y., GLASER P., GOFFEAN A., GOLIGHTLY E.J., GRANDI G.,
A GUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HERNUT A.,
JORIS B.Y., KARAMATA D., KASAHARA Y., KILAER-BLANCHARD M., KLEIN C.,
KOBAYSHI Y., KOETTER P., KONINGSTIN G., KROGH S.,
KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREYIC V.,
LEE S.M., LEVINE A., LIU H., MAGSIN S., MAUEL C., MEDIGUG C.,
MEDIAN N., MELLADO R.P., MILLOW M., NOBSKI M., MELLLY M., OGRAMA K., OGIWARA A., OUDEGA B., PARK S.H.,
NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
 -!- CATALYTIC ACTIVITY: CLEAVAGE OF 3-ASN-|-GLN-4, 9-SER-|-HIS-10 AND 14-ALA-LEU-15 BONDS IN INSULIN B CHAIN AND 14-TYR-|-GLN1-5 AND 8-ALA-|-SER-9 IN A CHAIN. CLEAVES TYPE IV COLLAGEN AT 258-ALA-|-GLN-259 IN ALPHA-1-(IV) AND AT 191-GLY-|-LEU-192 IN ALPHA-2-(IV).
 BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 -!- COFACTOR: ZINC.
EMBL: X91190; G995748; -.
PROSITE; PS00427; DISINTEGRINS; 1.
SIGRAL; HYDROLASE; BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
NON_TER 1
 Gaps
 HUANG K.F., HUNG C.C., PAN F.M., CHOW L.P., TSUGITA A., CHIOU S.H.; BIOCHEM. BIOPHYS. RES. COMMUN. 216:223-233(1995).
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
ATROLYSIN E PRECURSOR (EC 3 4.24.44) (CROTALUS ATROX
METALLOENDOPEPTIDASE E) (HEMORRHAGIC TOXIN E) (FRAGMENT).
TRIMERESURUS MUCROSQUAMATUS (TAIWAN HABU).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 ö
 Score 6; DB 12; Length 487;
Pred. No. 6.08e+00;
0; Mismatches 1; Indels
 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 24 POTENTIAL.
398 POTENTIAL.
54782 MW; 8477DBFF CRC32;
487 AA.
 487 AA
 CREATED)
 PRT;
 PRT;
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PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M., PRESEGAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., SCHLEICH S., SCHROFTER R., SCOFFONE F., SCHRÖTER R., SCOFFONE F., SERON S.J., SERROR P., SHIN B.S., SOLDO B., SOROKIN A., TACCONI E., TARRAIT H., TARRARAIN K., TARROCHI M., TANAKOSHI A., TANAKA T., TERFETRA P., TGONONI A., VANDENBOL M., VANNIER F., VASSAROTTI A., WANDUTT R., WEDLER E., WEDLER H., WASSHOTTI A., WINTERS P., WIPAT A., YAMMONTO H., YAMANDE K., YASHIKAMA H.F., ZUMSTEIN E., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.; NATURE 390:249-256(1997).
 UT 15
012678
012678
012679
012679
012679
012679
01-00-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
ALCOHOL ACETYLTRANSFERASE (EC 2.3.1.84) (ALCOHOL O-ACETYLTRANSFERASE)
 SYNECHOCYSTIS SP.
PROKARYOTA; BACTERIA; GRACILICUTES; OXYPHOTOBACTERIA; CYANOBACTERIA;
CHROOCOCCALES.
 Gaps
 Gaps
 ö
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 (AATASE).
LG-ATF1.
SACCHAROMYCES CARLSBERGENSIS (YEAST).
EUKARYOTA; PLANTAE; THALLOBIONTA; EUMYCOTA; HEMIASCOMYCETES;
 Score 6; DB 9; Length 521;
Pred. No. 6.08e+00;
0; Mismatches 0; Indels
 Score 6; DB 9; Length 487;
Pred. No. 6.08e+00;
 0; Indels
 STRAIN-AC327;
YAMANOTO H., UCHIYAMA S., NUGROHO F.A., SEKIGUCHI J.;
YAMANOTO H., UCHIYAMA S., NUGROHO F.A., SEKIGUCHI J.;
ENBL: 194:191-199(1997)
EMBL: 299108; E1182738; -.
EMBL: D86417; D1023184; -.
 KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 LT 14
052569
052569
055269
055269;
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 PROC. NATL. ACAD. SCI. U.S.A. 88:4275-4279(1991).
EMBL; D90288; G217097; -.
SEQUENCE 521 AA; 55453 MM; 25D2ED82 CRC32;
 56542 MW; 8F7FDAF2 CRC32;
 0; Mismatches
 Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
 Query Match
9.4%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 487 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. MEDLINE; 91239550.
 309 RYKGKE 314
 99
 11 LNAGTI 16
 32 LNAGTI 37
 61 RYKGKE
 STRAIN-168;
 ICTB GENE
 SEQUENCE
 SEQUENCE
 EMBL;
 RESULT
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 OSSEEDTAN
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STRAIN-KBIO01;
WADA M., YOSHIMOTO H., NAGASAWA N., BOGAKI T., TAMAI Y., HAMACHI M.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- CAFALYIIC ACTIVITY: ACETYL-COA + AN ALCOHOL - COA + AN ACETYL
 Gaps
 ö
 DB 1; Length 545; 6.08e+00; Indels
ENDOMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES
 EMBL, D63450; G939855; -.
TRANSFERASE; ACYLTRANSFERASE.
SEQUENCE 545 AA; 63246 MW; 4BE398B6 CRC32;
 0; Mismatches
 Score 6;
Pred. No.
 Search completed: Fri Sep 25 13:23:48 1998 Job time : 15 secs.
 Query Match 9.4%;
Best Local Similarity 100.0%;
Matches 6; Conservative
 SEQUENCE FROM N.A.
 73 LNDYCT 78
 46 LNDYCT 51
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| ********                             |                                        | *******                                 |
| *******                              |                                        | *******                                 |
| *                                    |                                        | **                                      |

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protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Fri Sep 25 13:18:51 1998; MasPar time 7.29 Seconds 387.265 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-20 (1-67) from PCTUS9816719A.pep 508 1 NSVHPCCDPVXCEPREGEHC......DYCTGISXDCPRNRYKGKED 67 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

140555 seqs, 42109429 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl6
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 33.312; Variance 51.559; scale 0.646 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|               |       | œ              |                          |   |          |                        |           |
|---------------|-------|----------------|--------------------------|---|----------|------------------------|-----------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | 8 | QI<br>QI | Description            | Pred. No. |
| -             | 386   | 76.0           | 478 1                    | 7 | 098995   | LEBETASE LE3 PRECURSOR | 9.78e-74  |
| 7             | 275   | 54.1           | 117 1                    | 2 | 090221   | PREPRO-HALYSTATIN 2 (F | 1.35e-45  |
| e             | 274   | 53.9           | 480 1                    | 2 | 090220   | PREPRO-HALYSTATIN PREC | 2.39e-45  |
| 4             | 248   | 48.8           | 706 1                    | 2 | 042593   | MEMBRANE ANCHORED META | 6.19e-39  |
| ស             | 231   | 45.5           | 115 1                    | 2 | 090222   | PREPRO-HALYSTATIN 3 (F | 8.58e-35  |
| Q             | 218   | 42.9           | 789 1                    | 9 | P70505   | FERTILIN ALPHA.        | 1.17e-31  |
| 7             | 217   | 42.7           | 481 1                    | 2 | 091505   | PRO-TRIMUCIN PRECURSOR | 2.04e-31  |
| 80            | 217   | 42.7           | 620 1                    | 2 | 042138   | METALLOPROTEINASE-DISI | 2.04e-31  |
| 9             | 215   | 42.3           | 150 1                    | 9 | 035674   | MELTRIN BETA, PARTIAL  | 6.14e-31  |
| 10            | 210   | 41.3           | 616 1                    | 2 | 090495   | ECARIN PRECURSOR.      | 9.63e-30  |
| 11            | 210   | 41.3           | 735                      | 7 | 028478   | FERTILIN BETA.         | 9.63e-30  |
| 12            | 210   | 41.3           | 735                      | 4 | 028472   | FERTILIN BETA.         | 9.63e-30  |
| 13            | 206   | 40.6           | 814                      | ~ | 013493   | MDC15.                 | 8.63e-29  |
| 14            | 206   | 40.6           | 814                      | ~ | 013444   | METARGIDIN PRECURSOR,  | 8.63e-29  |
| 15            | 202   | 40.4           | 735                      | N | P78326   | FERTILIN BETA (FRAGMEN | 1.49e-28  |
| 16            | 205   | 40.4           | 735                      | ~ | 596660   | FERTILIN BETA.         | 1.49e-28  |
| 17            | 203   | 40.0           |                          | 2 | 092119   | ATROLYSIN E PRECURSOR  | 4.45e-28  |
| 18            | 203   | 40.0           |                          | 2 | 012960   | ADAM 13.               | 4.45e-28  |
| 19            | 202   | 39.8           |                          | 2 | 060815   | A DISINTEGRIN AND META | 7.68e-28  |
| 20            | 200   | 39.4           | 600 1                    | 9 | Q60813   | FERTILIN ALPHA (PH-30  | 2.28e-27  |

| 2.28e-27               | 2.28e-27               | 3.93e-27               | 2.01e-26               | 3.45e-26           | 3.45e-26               | 3.45e-26 | 1.75e-25               | ,1.75e-25              | 3.00e-25 | 5.15e-25            | 5.15e-25         | 1.51e-24               | 4.43e-24           | 4.436-24              | 7.57e-24               | 7.57e-24               | 7.57e-24               | 3.77e-23               | 6.44e-23               | 1.10e-22               | 1.10e-22               | 5.42e-22     | 2.66e-21      | 2.66e-21        |
|------------------------|------------------------|------------------------|------------------------|--------------------|------------------------|----------|------------------------|------------------------|----------|---------------------|------------------|------------------------|--------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|--------------|---------------|-----------------|
| CATROCOLLASTATIN PRECU | FERTILIN ALPHA-II (FRA | CELLULAR DISINTEGRIN-R | HEMORRHAGIC TOXIN A (E | FERTILIN ALPHA'II. | FERTILIN ALPHA-I (FRAG | ALPHA-I. | FERTILIN ALPHA PROTEIN | MELTRIN, GAMMA PRECURS | ADAM7".  | TMDC VI (FRAGMENT). | METALLOPROTEASE. | FERTILIN ALPHA SUBUNIT | TMDC V (FRAGMENT). | PH-30 BETA PRECURSOR, | PUTATIVE METALLOPROTEI | EPIDIDYMAL APICAL PROT | METALLOPROTEASE/DISINT | FERTILIN ALPHA-I (FRAG | FERTILIN BETA PRECURSO | METALLOPROTEASE (FRAGM | EPIDIDYMAL APICAL PROT | PH-30 ALPHA. | TMDC II MRNA. | MELTRIN, ALPHA. |
| 090282                 | 019061                 | 060472                 | 092043                 | 028477             | 019056                 | 028476   | 019057                 | 061072                 | 035227   | P97778              | 090499           | 028659                 | P97777             | 260411                | 010718                 | 063180                 | 013443                 | 019060                 | 060718                 | 002060                 | 028475                 | 260410       | 028483        | 061824          |
| 12                     | 4                      | 2                      | 12                     | 4                  | 7                      | 4        | 4                      | 2                      | 10       | 12                  | 12               | 4                      | 12                 | 10                    | ~                      | 2                      | ~                      | 7                      | 10                     | 12                     | 4                      | 2            | 7             | 10              |
| 609                    | 792                    | 777                    | 419                    | 825                | 838                    | 905      | 836                    | 845                    | 788      | 81                  | 617              | 919                    | 203                | 735                   | 411                    | 789                    | 819                    | 821                    | 735                    | 549                    | 776                    | 804          | 756           | 903             |
| 39.4                   | 39.4                   | 39.2                   | 38.6                   | 38.4               | 38.4                   | 38.4     | 37.8                   | 37.8                   | 37.6     | 37.4                | 37.4             | 37.0                   | 36.6               | 36.6                  | 36.4                   | 36.4                   | 36.4                   | 35.8                   | 35.6                   | 35.4                   | 35.4                   | 34.8         | 34.3          | 34.3            |
| 200                    | 200                    | 199                    | 196                    | 195                | 195                    | 195      | 192                    | 192                    | 191      | 190                 | 190              | 188                    | 186                | 186                   | 185                    | 185                    | 185                    | 182                    | 181                    | 180                    | 180                    | 177          | 174           | 174             |
| 21                     | 22                     | 23                     | 24                     | 25                 | 56                     | 27       | 28                     | 29                     | 30       | 31                  | 32               | 33                     | 34                 | 35                    | 36                     | 37                     | 38                     | 39                     | 40                     | 41                     | 42                     | 43           | 44            | 45              |
|                        |                        |                        |                        |                    |                        |          |                        |                        |          |                     |                  |                        |                    |                       |                        |                        |                        |                        |                        |                        |                        |              |               |                 |

## ALIGNMENTS

| PRELIMINAR'  95  96  97  98-1997 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1999 (TREMBLREL. 0)  AN-1996 (TREMBLREL. 0)  AN-1999 (TREMBLREL. 0)  AN-1996 (TREMBLREL. 0)  AN-1996 (TREMBLREL. 0)  AN-1996 (TREMBLREL. 0)  AN-1996 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1999 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0)  AN-1999 (TREMBLREL. 0)  AN-1998 (TREMBLREL. 0) | PRELIMINARY; PRT; 478 AA.  298995  208995  208995  208995  101-FEB-1997 (TREMBLREL. 02, CREATED)  101-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  101-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  101-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  101-FEB-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)  101-FEB-1997 (TREMBLREL. 04)  101-FEB-1997 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  101-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  102-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  102-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  103-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  104-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  105-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  106-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  116-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  117-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  118-FEB-1997 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  119-FEB-1997 (TREMBLREL UPDATE)  101-FEB-1997 (TREMBLREL UPDATE) | Y; PRT; 117 AA.<br>1, CREATED)<br>1, LAST SEQUENCE UPDATE)<br>MENT). |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | SULT 1 098995 0198995 01-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUE 01-JAN-1998 (TREMBLREL. 05, LAST SEQUE MACROVIPERA LEBETINA (LEVANTINE VIPER) MACROVIPERA LEBETINA (LEVANTINE VIPER) 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | -1996<br>-1996<br>-1998<br>-HALYS                                    |

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 MEMBRANE ANCHORED METALLOPROTEASE, DISINTEGRIN, CYSTEINE-RICH PROTEIN
 55 PANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCNGISAGCPRNP 114
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 2 SVHPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRNR 61
 420 NPCCDAATCKLRQGAQCAEGLCCDQCRFMKKGTVCRIARGDDMDDYCNGISAGCPRNPF 478
 Gaps
 Gaps
 TISSUE-LIVER;
FUJISAMA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
FRATEDA KENKYUSHO HO 53:39-56(1994).
EMBL; D28871; G559298; -.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
 SEQUENCE FROM N.A.

TISSUE-WENDM GLAND;
FUJISSMAY Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
FUJISMAY Y. AURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.;
TAKEDA KENKYUSHO HO 53:39-56(1994).
FRBIL: DS8870; G465190; ---
PROSITE: PSO0427; DISIMPEGRINS; 1.
SIGNAL: BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
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EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
 AGKISTRODON HALYS.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
 TISSUE-TESTIS;
SHILLING F.M., KRAETZSCHMAR J, GAYKO U., CAI H., WESKAMP G.
LEIBOW L., MYLES D.G., NUCCITELLI R., BLOBEL C.P.;
 Length 117;
 Length 480;
 Ouery Match 54.1%; Score 275; DB 12; Length 11
Best Local Similarity 47.5%; Pred. No. 1.35e-45;
Matches 29; Conservative 11; Mismatches 21; Indels
 12; Mismatches 19; Indels
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPRO-HALYSTATIN PRECURSOR.
 Score 274; DB 12;
Pred. No. 2.39e-45;
 NON_TER 1 1 1 SEQUENCE 117 AA; 12686 MW; 15139DFC CRC32;
 68983596 CRC32;
 480 AA
 706 AA
 POTENTIAL.
 POTENTIAL
 POTENTIAL
 PRT;
 PRT;
 53619 MW;
 PRELIMINARY;
 PRELIMINARY;
 Similarity 47.5%;
28; Conservative
 18
 480
 480 AA;
 Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 115 F 115
 62 Y 62
 SEQUENCE
 Query Match
 LT 3
Q90220
Q90220;
 LT 4
042593
042593;
 SIGNAL
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 Matches
 RESULT
 RESULT
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407 SCCDPTSCKLRENGECLTGLCCKDCKLLPRGTLCRMPKTECDLAEYCDGASNHCPLDMYK 466
 464 HPCCEPT-CTLKVGAQCSEGLCCYKCTFKKKGTLCRPAEDVCDLPEYCNGITGECPANSY 522
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAM-LDGLNDYCTGISXDCPRNRX 62
 55 PANPCCDAATCKLRPGAQCAEGLCCDQCRFIKAGTVCRRARGDWNDNTCTGQSADCPRN 113
 Gaps
 2 SVHPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRN 60
 FUJISAWA Y., KURODA S.I., NOTOYA K., KONISHI H., TERASHITA Z.I.; TAKEDA KENKYUSHO HO 53:39-56(1994).
EMBL; D28871; 6559299;
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
 RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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 ;
 'n
 AGKISTRODON HAITS.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILLA;
LEPIDOSAURIA; SQUAMATA; SERPENTES; CULOBROIDEA; VIPERIDAE.
 Length 115;
 Length 706;
 Length 789;
 21; Indels
 20; Indels
 Indels
 SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y08616; E274094; -.
SPERM; TRANSMEMBRANE.
SEQUENCE 789 AA; 86140 MW; 242203E2 CRC32;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U78185; G2231331; -.
INTERIN; PROTEASE; METALLOPROTEASE.
SEQUENCE 706 AB, 79275 MM; 8992584A CRC32;
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PREPRO-HALL'STATIN 3 (FRAGMENT).
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 Score 248; DB 12;
Pred. No. 6.19e-39;
13; Mismatches 20
 Score 231; DB 12;
Pred. No. 8.58e-35;
 Score 218; DB 10;
Pred. No. 1.17e-31;
 115 AA; 12389 MW; C10C6FAF CRC32;
 12; Mismatches
 11; Mismatches
 115 AA
 STRAIN-SPRAGUE DAWLEY; TISSUE-TESTIS;
 PRT;
 PRT;
 ULT 6
P70505
P70505
01-FEB-1997 (TREMBLREL. 02, CR 01-FEB-1997 (TREMBLREL. 02, LA 01-FEB-1997 (TREMBLREL. 02, LA
 PRELIMINARY;
 Query Match 48.8%;
Best Local Similarity 43.3%;
Matches 26; Conservative
 Query Match 45.5%;
Best Local Similarity 47.5%;
 Query Match 42.9%;
Best Local Similarity 42.6%;
Matches 26; Conservative
 28; Conservative
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 FERTILIN ALPHA
 TISSUE-LIVER;
 NON_TER
SEQUENCE
 523 M 523
 LT 5
090222
090222;
 Matches
 RESULT
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 427 NPCCDAATCKLTPGSQCADGVCCDQCRFTRAGTECRQAKDDCDMADLCTGQSAECPTDRF 486
 Gaps
 421 NPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRCTGQSADCPRN 477
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLDGLNDYCTGISXDCPRN 60
 SEQUENCE FROM N.A.

DE ARAUJO H.S., OWNBY C.L.;

SUBMITTED (JAN-1299) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; U86634; G2231613; --

PROSITE; PS00427; DISINTEGRINS; 1.

INTEGRIN; HYDROLASE; BLOOD COAGULATION; PLATELET; CELL ADHESION;
 Score 217; DB 12; Length 620;
Pred. No. 2.04e-31;
10; Mismatches 23; Indels 1;
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
METALLOPROTEINASE-DISINTEGRIN-LIKE PROTEIN (EC 3.4.24.1).
AGKISTRADON CONTORRIX LATICINCTUS.
EUKARYOTA: METALOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
PRO-TRIMUCIN PRECURSOR.
TRIMERESURUS MUCROSQUAMATUS (TAIWAN HABU).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 ö
 Length 481;
 7; Mismatches 22; Indels
 [2]
SEQUENCE FROM N.A.
SEQUENCO H.S., OWNBY C.L.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 Score 217; DB 12;
Pred. No. 2.04e-31;
 PRO-TRIMUCIN.
23A332F0 CRC32;
 OFEODOIA CRC32;
 481 AA
 MEDLINE; 95314311.
DE ARAUJO H.S., OWNBY C.L.;
ARCH. BIOCHEM. BIOPHYS. 320:141-148(1995).
 PRT;
 1 18 PC
19 481 PF
481 AA; 54079 MW;
 620 AA; 69512 MW;
 PRELIMINARY;
 Match 42.7%;
Local Similarity 43.3%;
les 26; Conservative
 PRELIMINARY;
 Query Match 42.7%;
Best Local Similarity 49.1%;
Matches 28; Conservative
 SEQUENCE FROM N.A. MEDLINE; 95314311.
 SEQUENCE
63
 SEQUENCE
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091505;
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ID 042138
AC 042138;
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 429 NPCCDAATCKLKPGAECGNGECCDKCKIRKAGTECRPARDDCDVAEHCTGOSAECPRNEF 488
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLD-GLNDYCTGISXDCPRNRX 62
 4 HPCCDPVXCEPREGEHCISGPCCRNCKFLNAGTICKXAMLD-GLNDYCTGISXDCPRNRY 62
 13 NPCCNASNCTLKEGAECAHGSCCHQCKLVAPGTQCREQVRQCDLPEFCTGKSPHCPTNYY 72
 Gaps
 Gaps
 SEĞUENCE FROM N.A.
MEDLINE; 96026308.
YAĞAMI-HIROMASA T., SATO T., KURISAKI T., KAMIJO K., NABESHIMA Y.,
 MORITA T., TAKEYA H.,
 1;
 ECHIS CARINATUS (SAW-SCALED VIPER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 MGI:105377.
MGS MGSCULUS (MOUSE).
EUKRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
 ä
 MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 Length 616;
 Length 150;
 Query Match
41.3%; Score 210; DB 12; Length 616
Best Local Similarity 43.3%; Pred. No. 9.63e-30;
Matches 26; Conservative 12; Mismatches 21; Indels
 Score 215; DB 10; Length 15
Pred. No. 6.14e-31;
14; Mismatches 21; Indels
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-0AN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
FERTILIN BETA.
 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
MELTRIN BETA, PARTIAL CDS (FRAGMENT).
 150 AA; 16395 MW; E8B6AAFC CRC32;
 191 616 ECARIN.
616 AA; 69462 MW; DE2FC9AA CRC32;
 SEQUENCE FROM N.A.
TISSUB-VENOMOUS GLAND;
MISHIDA S., FUJITA T., KOHNO N., ATODA H., MOI
KIDO I., PAIRE M.J., KAWABATA S., IWANAGA S.;
ENDL. 1., PAIRE M.J., KAWABATA S., IWANAGA S.;
EMBL. D32212; G717091; -.
 616 AA
 Ş
 POTENTIAL.
ECARIN.
 PRT;
 PRELIMINARY; PRT;
 FUJISAWA-SEHARA A.;
NATURE 377-652-656(1995).
EMBL, D50410; G1125028. --
MGD; MGI:105377; MGI:105377.
 PRELIMINARY;
 PRELIMINARY;
 Ouery Match
Best Local Similarity 40.0%;
Matches 24; Conservative
 18
616
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 ECARIN PRECURSOR.
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442 DCVDPCCDSLTCQLRPGAQCASDGPCCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQCP 501
 413 CCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHY 470
TISSUE-TESTIS;
MEDLINE; 97224507.
MEDLINE; 97224507.
GENCKIN H.R., BURKIN D.J., DAVEY P.M., GRIFFIN D.K., AFFARA N.A.;
GENOMICS 40.190-192(1997).
EMBL; X99374; E254267; -..
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
 6 CCDPVXCEPREGEHCISGPCCRNCKFLNAGIICKXAMLD-GLNDYCTGISXDCPRNRY
 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
 01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
FERTILIN BETA (FRAGMENT).
FUNDO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; BUTHBRIA; PRIMATES.
 10; Mismatches 24; Indels
 21; Indels
 01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
 Score 205; DB 2; I
Pred. No. 1.49e-28;
 Score 206; DB 2; 1
Pred. No. 8.63e-29;
 28 POTENTIAL.
814 METARGIDIN.
87686 MW; 9767B2E0 CRC32;
 735 AA; 82533 MW; C10E2582 CRC32;
 14; Mismatches
 814 AA
 735 AA
 SEQUENCE FROM N.A.
KRAETZSCHAAR J.R., LUM L., BLOBEL C.P.,
J. BIOL. CHEM. 271.4593-4596(1996).
EMBL: U41767; G1235674;
 Search completed: Fri Sep 25 13:19:10 1998
 PRT;
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 Query Match 40.4%;
Best Local Similarity 39.7%;
Matches 23; Conservative
 40.6%;
Local Similarity 40.3%;
les 25; Conservative
 01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
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 METARGIDIN PRECURSOR
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814 AA;
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 442 DCVDPCCDSLTCQLRPGAQCASDGPCCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQCP 501
 413 CCDTATCRFKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGTSASCPENHF 470
 413 CCDTATCRFKAGSNCAEGPCCENCLFMSQERVCRPSFDECDLPEYCNGTSASCPENHF 470
 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
 1;
 MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
EUTHERIA; PRIMATES.
 5
 Length 735;
 Length 814;
 Length 735;
 Query Match 40.6%; Score 206; DB 2; Length 814 Best Local Similarity 40.3%; Pred. No. 8.63e-29; Matches 25; Conservative 14; Mismatches 21; Indels
 24; Indels
 24; Indels
 SEQUENCE FROM N.A.
RAMARAO C.S., WHITE J.M., PRIMAKOFF P.;
RAMARAO (S.S. MYLES D.G., WHITE J.M., PRIMAKOFF P.;
BUBLITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U33959; G998340; --
PROSITE; PSOM427; DISINVEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SECUENCE 735 AA; 82372 MW; 8E68BAC9 CRC32;
 C28472 PRELIMINARY; PRT; 735 AA. 028472; 000472; 010V-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 PERRY A.C.F., GICHUHI P.M., JONES R., HALL L.;
BIOCHEM. J. 307:843-850(1995).
BENBL; X77653; G794077; -.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SEQUENCE 735 AA; 82358 MW; F31BBC91 CRC32;
 Score 210; DB 4; 1
Pred. No. 9.63e-30;
11; Mismatches 24;
 Query Match 41.3%; Score 210; DB 4; 1
Best Local Similarity 37.9%; Pred. No. 9.63e-30;
Matches 22; Conservative 11; Mismatches 24,
 HERREN B., RAINES E.W., ROSS R.;
FASEB J. 11:173-180(1997).
BEREJ: U46005; G1338972; --
SEQUENCE 814 AA; 87716 MW; AZABFEZF CRC32;
 814 AA
 PRT;
 01,
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05,
 PRELIMINARY;
 Query Match 41.3%;
Best Local Similarity 37.9%;
Matches 22; Conservative
 01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
MDC15.
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 TISSUE-UMBILICAL VEIN; MEDLINE; 97192141.
 EUTHERIA; PRIMATES
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE-TESTIS;
MEDLINE; 95260313
 FERTILIN BETA.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Sep 25 13:22:32 1998; MasPar time 4.55 Seconds 369.383 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-20 (1-67) from PCTUS9816719A.pep 64

1 NSVHPCCDPVXCEPREGEHC.....DYCTGISXDCPRNRYKGKED Description: Perfect Score: Sequence:

TABLE unitprotable Gap 60 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match O% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 2.924; Variance 0.349; scale 8.380 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Pred. No.           | 1.01e-12               | 1.09e-02               | 1.09e-02               | 1.09e-02              | 1.09e-02               | 1.09e-02               | 1.09e-02              | 1.09e-02               | 1.09e-02               | 1.41e+00               | 1.41e+00               | 1.41e+00               | 1.41e+00              | 1.41e+00               | 1.41e+00               | 1.41e+00               | 1.41e+00              | 1.41e+00               | 1.41e+00              | 1.41e+00               | 1.41e+00              | 1.41e+00              | 1.41e+00       |  |
|---------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|-----------------------|------------------------|-----------------------|-----------------------|----------------|--|
| Description         | DISINTEGRIN ECHISTATIN | DISINTEGRIN BATROXOSTA | DISINTEGRIN VIRIDIN (P | DISINTEGRIN CEREBERIN | DISINTEGRIN COTIARIN ( | DISINTEGRIN MOLOSSIN ( | DISINTEGRIN JARARACIN | PROBABLE APOPTOSIS INH | RIBOSE-PHOSPHATE PYROP | DISINTEGRIN ERISTICOPH | DISINTEGRIN FLAVOSTATI | DISINTEGRIN CROTATROXI | DISINTEGRIN BASILICIN | DISINTEGRIN LUTOSIN (P | DISINTEGRIN LACHESIN ( | DISINTEGRIN CERASTIN ( | DISINTEGRIN ELEGANTIN | DISINTEGRIN TERGEMININ | DISINTEGRIN BARBOURIN | PROBABLE RNA POLYMERAS | UL45 HOMOLOG PROTEIN. | UL45 HOMOLOG PROTEIN. | SRG-3 PROTEIN. |  |
| er<br>er            | DISI_ECHCA             | DISI_BOTAT             | DISI_CROVV             | DISI_CROVE            | DISI_BOTCO             | DISI_CROMM             | DISI_BOTJA            | IAP2_NPVAC             | KPRS_HELPY             | DISLERIMA              | DISI_TRIFL             | DISI_CROAT             | DISI_CROBA            | DISI_CROVL             | DISI_LACMU             | DISI_CROCC             | DISI_TRIEL            | DISI_SISTE             | DISI_SISBA            | FECI_ECOLI             | UL45_HSVMB            | UL45_HSVMM            | SRG3_CAEEL     |  |
| 60                  | -                      | -                      | -                      | -                     |                        | Н                      | Н                     | -                      | Н                      | -                      | -                      | ٦                      | ч                     | -                      | -                      | -                      | П                     | П                      | -                     | -                      | П                     | ч                     | Н              |  |
| Length              | 49                     | 71                     | 71                     | 72                    | 72                     | 73                     | 73                    | 249                    | 318                    | 51                     | 99                     | 72                     | 72                    | 73                     | 73                     | 73                     | 73                    | 73                     | 73                    | 173                    | 211                   | 211                   | 332            |  |
| å<br>Query<br>Match | 17.2                   | 10.9                   | 10.9                   | 10.9                  | 10.9                   | 10.9                   | 10.9                  | 10.9                   | 10.9                   | 9.6                    | 9.4                    | 9.4                    | 9.4                   | 9.4                    | 9.4                    | 9.4                    | 9.4                   | 4.6                    | 9.4                   | 9.6                    | 9.4                   | 9.4                   | 9.4            |  |
| Score               | 11                     | 7                      | 7                      | 7                     | 7                      | 7                      | 7                     | 7                      | 7                      | ø                      | ø                      | ø                      | φ                     | 9                      | ø                      | φ                      | ø                     | ø                      | 9                     | Q                      | 9                     | ø                     | 9              |  |
| Result<br>No.       | П                      | 7                      | m                      | 4                     | S                      | 9                      | 7                     | æ                      | σ                      | 10                     | 11                     | 12                     | 13                    | 14                     | 15                     | 16                     | 17                    | 18                     | 19                    | 20                     | 21                    | 22                    | 23             |  |

STRUCTURE BY NMR. MEDLINE; 92089067

| 1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.41e+00<br>1.4 |
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| ULTRASPIRACLE PROTEIN HEMORRHAGIC METALLOPRO 5-HYDROXYTRYPTAMINE 2B 5-HYDROXYTRYPTAMINE 2B 5-HYDROXYTRYPTAMINE 2B NADH-PLASTOQUINONE OXI PLACENTAL FOLATE TRANS HYPOTHETICAL 6B.3 KD P TOPOISOMERASE IV SUBUN PROTEIN 01. PROTHETICAL 86.3 KD P HYPOTHETICAL 93.1 KD P LARGE TEGUMENT PROTEIN LARGE TEGUMENT PROTEIN CAD PROTEIN (CONTAINS: HYPOTHETICAL 27.1 KD P INSERTION ELEMENT IS63 PROBABLE G PROTEIN COD HYPOTHETICAL 27.1 KD P HYPOTHETICAL 79.4 KD P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| USP_MANSE<br>HRTE_CROAT<br>5H2B_HUWAN<br>5H2B_HUWAN<br>YG4B_ETOAT<br>PARE_SALTY<br>VOOL_VARV<br>VOOL_VARV<br>VOOL_VARV<br>VOOL_VARV<br>VATA_SCHPO<br>YL34_YEAST<br>TEGU_HSVG<br>PALL_SOLTU<br>VYRD_HAETN<br>YR34_YEAST<br>TEGU_HSVG<br>PRIJ_BROWE<br>YH34_YEAST<br>TEGU_HSVG<br>PRIJ_BROWE<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EOLLI<br>YH36_EARET                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| аннананнананнан                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 75000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| $\begin{array}{cccccccccccccccccccccccccccccccccccc$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| กเนนนออออออออออออออออออออออ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 40000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

### ALIGNMENTS

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 p17347;
1-A0G-1990 (REL. 15, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DISINTEGRIN ECHISTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
 MEDLINE; 92104151.
COOKE R.M., CARTER B.G., MARTIN D.M.A., MURRAY-RUST P., WEIR M.P.;
EUR. J. BIOCHEM. 202:323-328(1991).
 TISSUE-VENOM;
MEDILINE; 89066819.
MADILINE; 800LD R.J., JACOBS J.W., FRIEDMAN P.A., POLOKOFF M.A.;
J. BIOL. CHEM. 263:19827-19832(1988).
 STRUCTURE BY NMR.
MEDLINE; 92104150.
DALVIT C., WIDMER H., BOVERMANN G., BRECKENRIDGE R., METTERNICH
EUR. J. BIOCHEM. 202:315-321(1991).
 TISSUE-VENOM;
MEDLINE; 90207217.
MEDLINE; 90207217.
DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZAROS R.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
 (CARINATIN).
ECHIS CARINATUS (SAW-SCALED VIPER).
EUKRAYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAORIA; SERPEMTES.
 MEDLINE; 92104152.
SAUDEK V., ATKINSON R.A., LEPAGE P., PELTON J.T.;
EUR. J. BIOCHEM. 202:329-338(1991).
 49 AA.
 STRUCTURE BY NMR.
MEDLINE, 9130B124.
MEDRINE, ATKINSON R.A., PELTON J.T.;
BIOCHEMISTRY 30:7369-7372(1991).
 PRT;
 STANDARD;
 STRUCTURE BY NMR
 STRUCTURE BY NMR
RESULT 1
DISTECTION
DO 11347;
DT 01-AUG-1990
DT 01-FEB-1995
DE 01SINTEGRIN
DE (CARINATIN).
OS ECHRICARININ).
OS ECHRICARININ.
OC EURARYOTA; IN
RP SEQUENCE.
RC TISSUE-YENO!
RA GAN 2.R. 9
RA GAN 2.R. 1
RA DEISHER T.R. 8
RA SAUDER V. 1
RA SAUDER V. 1
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RA STRUCTUR
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SEQUENCE
 SEQUENCE
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 DISULFID
 Query Match
 54
 62
 54
 Matches
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 RESULT
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 MEDLINE; 91002685.

RUCINSKI B., NIEWIAROWSKI S., HOLT J.C., SOSZKA T., KNUDSEN K.A.;
BIOCHINE BIOPHYS. ACTA 1054:257-262(1990).
-!-FUNCTION: INHIBITS FIBERINGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
 FEBS LETT. 309:316-320(1992).

-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS

-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS

EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE

GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT

AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 DISINTEGRIN BATROXOSTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS ATROX (BARBA AMARILLA) (FER-DE-LANCE).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROFEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM. PIR; $13168; $13168.
 PDB; 2ECH; 31-OCT-93.
PROSTIE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM; 3D-STRUCTURE.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (IN ALPHA-2
 Gaps
 THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
7 A32029: A32029.
CHEN Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL G.,
 ö
 MEDLINE; 92387379.
CALVETE J.J., WANG Y., MANN K., SCHAEFER W., NIEWIAROSKI S.,
 Indels
 Score 11; DB 1; Length 49;
Pred. No. 1.01e-12;
0; Mismatches 0; Indels
 CELL ATTACHMENT SITE.
MISSING (IN ALPHA-2 FORM).
 BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM
 01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 0A851E33 CRC32;
 71 AA.
 FORM).
PROBABLE.
 PROBABLE
 PRT;
 HSSP; P17494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
 BAUM J.;
BIOCHEMISTRY 30:11625-11636(1991)
 5424 MW;
 Local Similarity 100.0%;
les 11; Conservative
 17.28;
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 A35982; A35982,
S29198; S29198
 22 SGPCCRNCKFL 32
 4 SGPCCRNCKFL 14
 AA;
 AND COLLAGEN.
 DISULFIDE BONDS
 STEWART G.J.;
 LT 2
DISI_BOTAT
P18618;
 DISULFID
DISULFID
DISULFID
 SEQUENCE.
 SEQUENCE
 DISULFID
 Query Match
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Matches
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MEDLINE; 93123215.

XX MEDLINE; 93123215.

XA SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,

RA NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;

XI J. BIOL. CHEM. 268:1058-1065(1993).

YENTIAL L. PONCTION: INHIBITS FIRSTNOGEN INTERACTION WITH PLATELET RECEPTORS

CINCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND

INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING

CINCOPROTEIN ISB-INTEGRINS ON THE PLATELET SURFACE AND

INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING

EACTOR AND COLLAGEN.

C. -1- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN

ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.

PROSITE; PROG17: DISINTEGRINS; 1.
 ö
 ö
 MEDLINE; 9312315.
SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
SCARBOROUGH R.M., ROSE J.W., RAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-!- FUNCTION: INHIBITE FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
 Gaps
 Gaps
 DISI_CROVE STANDARD; PRT; 72 AA.
P31985;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN CEREBERIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS VIRIDIS CEREBERUS (ARIZONA BLACK RATLESNAKE).
EUKARNOTA; METAZOA; CHONDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 UL-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DISINTEGRIN VIRDIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS VIRIDIS (PRAIRIE RATLESNAKE).
EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; TETRAPODA; REPTILLA;
 ô
 PROSTIE: PS010.27: DISINTEGRINS; 1.

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

SITE 50 52 CELL ATTACHMENT SITE (POTENTIAL).

SEQUENCE 71 AA; 7637 MW; 910AF02C CRC32;
 ö
 1; Indels
 1; Indels
 DB 1; Length 71;
1.09e-02;
 DB 1; Length 71;
1.09e-02;
 CELL ATTACHMENT SITE. A73CFB7E CRC32;
 71 AA.
 Mismatches
 Mismatches
 BY SIMILARITY
 Score 7;
Pred. No.
 .
Ю
 Score 7;
 PRT;
 Pred.
 66
53
7602 MW;
 10.9%;
ilarity 87.5%;
Conservative
 10.98;
 arity 87.5%;
Conservative
 STANDARD;
 LEPIDOSAURIA; SERPENTES
 Query Match
Best Local Similarity
47
51
71 AA;
 Local Similarity
 63 SADCPRNR 70
 SADCPRNR 69
 SXDCPRNR 61
 SXDCPRNR 61
 TISSUE-VENOM;
 DISI_CROVV
P31987;
01-JUL-1993 (
01-JUL-1993 (
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Query Match
 Query Match
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 INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 INHIBITS AND COLLEGEN.

FACTOR AND COLLEGEN.

-1- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; F43019; F43019; F43019.
HSSP; P17494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
BISULFID 47 66
BY SIMILARITY.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL).
INHIBITS AGGREGATE.

FACTOR AND COLLAGEN.

-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIRS; B43020; B43020.
HSSP; P17494; IKST.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGUATION; PLATELET; CELL ADHESION; VENOM.
SITE
51
53
CELL ATTACHMENT SITE (POTENTIAL).
SITE.
77 AA: 7781 MW; BFE2B942 CRC32;
 Gaps
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DISINTEGRIN COTIARIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS COTIARA (COTIARA).
EUKARYOTA; METAZOA; CHONDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 DISI_CROMM STANDARD; PRT; 73 AA.
P$1984;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
COTALUS MOLOSSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS MOLOSSUS MOLOSSUS (NORTHERN BLACK-TAILED RATLLESNAKE).
EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA: SERPENTES.
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 e 7; DB 1; Length 72;
. No. 1.09e-02;
Mismatches 1; Indels
 1; Indels
 Length 72;
 Score 7; DB 1; Le
Pred. No. 1.09e-02;
 72 AA.
 0; Mismatches
 Score 7;
Pred. No.
0; Mismal
 PRT;
 10.9%;
llarity 87.5%;
Conservative
 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
 STANDARD;
 Local Similarity
 63 SADCPRNR 70
 SADCPRNR 70
 54 SXDCPRNR 61
 SXDCPRNR 61
 TISSUE-VENOM;
 DISI_BOTCO
P31988;
 [1]
SEQUENCE.
 SEQUENCE
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 63
 54
 Matches
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 SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARFSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1055(1993).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROFIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARESTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-1- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACTS BY BINDING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
 INHIBLY: ACCREMENT.
FACTOR AND COLLEGEN.
-!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; H43019, 143019.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
73 AA: 7880 MW; 7312E08D CRC32;
 -1- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIS, 44320.0, 443020.
PROSITE; PSO0427; DISINTEGRINS; 1.
PROSITE; PSO0427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
47 66 BY SIMILARITY.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL).
SEQUENCE 73 AA; 7739 MW; 15EEAA7A CRC32;
 Gaps
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN JARARACIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
BOTHROPS JARARACA (JARARACA).
EUKANYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
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 1; Indels
 1; Indels
 Length 73;
 DB 1; Length 73;
1.09e-02;
 DB 1; Ler
1.09e-02;
 Score 7; DB 1;
Pred. No. 1.09e-(
0; Mismatches
 Score 7; DB 1;
Pred. No. 1.09e-
0; Mismatches
 249 AA.
 73 AA
 PRT;
 PRT;
 TAP2_NPVAC STANDARD;
P41454;
01-NOV-1995 (REL. 32, CREATED)
 10.9%;
larity 87.5%;
Conservative
 10.9%;
larity 87.5%;
Conservative
 STANDARD;
 FACTOR AND COLLAGEN.
 Local Similarity
 SEQUENCE.
TISSUE-VENOM;
MEDLINE; 93123215.
 Local Similarity
93123215.
 63 SADCPRNR 70
 63 SADCPRNR 70
 54 SXDCPRNR 61
 SXDCPRNR 61
 7
DISI_BOTJA
P31989;
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Matches
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 VEWTER J.C.;
NATURE 388:539-547(1997).

-! CATALYIIC ACTIVITY: ATP + D-RIBOSE 5-PHOSPHATE = AMP +
-! CATALYIIC ACTIVITY: ATP + D-RIBOSE 1-DIPHOSPHATE.
-! COPACTOR: BOTH INORGANIC PHOSPHATE AND MAGNESIUM ION ARE REQUIRED
FOR ENZYME STABILITY AND ACTIVITY (BY SIMILARITY).
-! PATHWAY: THIS ENZYME IS UTILIZED BY BOTH THE DE NOVO & THE SALVAGE
PATHWAYS BY WHATE ENDOSENOUSLY FORMED OR EXCRENOUSLY ADDED
PYRIMIDINE, PURINE, OR PYRIDINE BASES ARE CONVERTED TO THE
CORRESPONDING RIBONICLEOSIDE MONOPHOSPHATES (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE
 TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCANNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKI M., KARP P.D., SMITH H.O., FRASER C.M.,
 Gaps
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.
 STRAIN-C6;

BEDLINE; 94303173.

AYRES M.D. HOWARD S.C., KUZIO J., LOPEZ-FERBER M., POSSEE R.D.;

VIROLGGY 202:586-605(1994).

-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

BRBL: L25858; G559140; -.

PROSITE: PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.
 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) (PHOSPHORIBOSYL
 ő
 0; Indels
 Length 249;
 BIOSYNTHESIS; TRANSFERASE; KINASE; MAGNESIUM
 WAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
 Score 7; DB 1; Le
Pred. No. 1.09e-02;
0; Mismatches 0
 C3HC4-TYPE.
840DE2A2 CRC32;
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE APOPTOSIS INHIBITOR 2 (IAP-2).
 318 AA.
 HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
 PS00114; PRPP_SYNTHETASE; 1.
 PRT;
 249 AA; 28621 MW;
 34824 MW;
 Query Match 10.9%;
Best Local Similarity 100.0%;
Matches 7; Conservative
 PYROPHOSPHATE SYNTHETASE).
 STANDARD;
 139
148
 152
318 AA;
 MEDLINE; 97394467.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCKFLNA 153
 139
 NCKFLNA 34
 PRSA OR HP0742
 STRAIN-26695
 IGR; HP0742
 NUCLEOTIDE
 KPRS_HELPY
 ZN_FING
SEQUENCE
 METAL
SEQUENCE
 PROSITE;
 METAL
 147
 28
 RESULT
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 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DISINTEGRIN FLAVOSTATIN (RGD-CONTAINING PEPTIDE) (PLATELET AGGREGATION
 MEDLINE; 97269274.

MARUTAMA K., KAWASAKI T., SAKAI Y., TANIUCHI Y., SHIMIZU M.,

KAWASHIMA H., TAKENAKA T.;

PEPTIDES 18:73-78(1997).

-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS

EXPRESSED ON GLYCOPROPIEN IIB-IIIB-IIG COMPLEX. ACT BY BINDING TO THE

GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT

AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 SCREBOROUGH R.M., ROSE J.W., HSU M.A., PHILLIPS D.R., FRIED V.A., CAMPBELL A.M., NANNIZZI L., CHARO I.F.;
J. BIOL. CHEM. 266:9359-9362(1991).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROFIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROFIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
 01-AUG-1991 (REL. 19, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DISINTPERRIN ERISTICOPHIN (PLATELET AGREGATION ACTIVATION INHIBITOR).
ERISTOCOPHIS MACMADINI (LEAF-NOSED VIPER).
ERISTOCO, METAZOA, CHORDATA, VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 Gaps
 Gaps
 -!- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR; C40003, C40003.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
 TRIMBRESURUS FLAVOVIKIDIS (HABU).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 ö
 ö
 PYRROLIDONE CARBOXYLIC ACID.
 0; Indels
 1; Indels
 Length 318;
 Length 51;
 BY SIMILARITY.
CELL ATTACHMENT SITE.
119C037C CRC32;
 Score 7; DB 1; Le
Pred. No. 1.09e-02;
 Score 6; DB 1; Le
Pred. No. 1.41e+00;
 0; Mismatches
 0; Mismatches
 68 AA
 51 AA
 PRT;
 5823 MW;
10.9%;
similarity 87.5%;
7; Conservative
 Query Match 9.4%;
Best Local Similarity 100.0%;
 6; Conservative
 STANDARD;
 STANDARD;
 ACTIVATION INHIBITOR
 Query Match
Best Local Similarity
 TISSUE-VENOM;
MEDLINE; 91236695.
 51 AA;
 233 AGTICKAA 240
 AND COLLAGEN.
 34 AGTICKXA 41
 39
 TISSUE=VENOM;
 DISI_TRIFL
P80949;
 34 NDYCTG
 LT 10
DISI_ERIMA
P22826;
 MOD_RES
DISULFID
 SEQUENCE
 SEQUENCE
 SEQUENCE
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S

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54 SXDCPRN 60
 9
 62 SADCPRN 68
 63 SADCPRN 69
 TISSUE-VENOM;
 DISI_CROVL
P31986;
 SEQUENCE
 Query Match
 SEQUENCE
 Query Match
 15
 HSSP;
 Matches
 Matches
 Best
 RESULT
 RESULT
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 -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROFEIN
ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR: B43019; B43019.
HSSP; P17494; IKST.
PROSITE; PS00427; DISINTEGRINS; 1.
PROSITE; PS00427; DISINTEGRINS; 1.
SILCO COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE
51 53 CELL ATTACHERNT SITE (POTENTIAL).
SEQUENCE 72 AA; 7521 MW; 77411CCE CRC32;
 Gaps
 Gaps
 -1- SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PROSITE; PSO0427; DISINTEGRINS, 1.

BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
DISULEID 6 14 BY SIMILARITY.
DISULEID 27 57 BY SIMILARITY.
DISULEID 27 57 BY SIMILARITY.
DISULEID 32 36 BY SIMILARITY.
DISULEID 32 36 BY SIMILARITY.
DISULEID 45 64 BY SIMILARITY.
SITE 47 49 CELL ATTACHENT SITE (POTENTIAL).
SEQUENCE 68 AA; 7316 MW; 35C79AIC CRC32;
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN BASILICIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANOMATION UPDATE)
DISINTEGRIN CROTATROXIN/DURISSIN (PLATELET AGGREGATION ACTIVATION
 CROTALUS ÁTROX (WESTERN DIAMONDBACK RATTLESNAKE), AND CROTALUS DURISSUS DURISSUS (CENTRAL AMERICAN RATTLESNAKE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAUKIA; SERPENTES.
 ö
 ö
 1; Indels
 1; Indels
 Score 6; DB 1; Length 72;
Pred. No. 1.41e+00;
0; Mismatches 1; Indel.
 Length 68;
 Score 6; DB 1; Le
Pred. No. 1.41e+00;
0; Mismatches 1
 72 AA
 72 AA
 PRT;
 PRT;
 9.48;
 9.4%;
 Conservative
 6; Conservative
 STANDARD;
 STANDARD;
 Ouery Match
Best Local Similarity
Matches 6; Conser
 lest Local Similarity
Matches 6; Conser
 SXDCPRN 60
 SXDCPRN 60
 61 SADCPRN 67
 SADCPRN 68
 IISSUE-VENOM;
 LI 13
DISI_CROBA
P31981;
 DISI_CROAT
P31980;
 Match
 SEQUENCE
 54
 62
 54
 RESULT
 RESULT
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 TISSUE-VENOM;
MEDLINE; 9312315.
SCARBORDGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,
NANNIZZI L., ARRSTEN A., CAMPBELL A.M., CHARO I.F.;
J. BIOL. CHEM. 268:1058-1065(1993).
-1- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROTEIN ILB-IIIA COMPLEX. ACTS BY BIRNING TO THE
GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SUPPACE AND
INHIBITS AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
FACTOR AND COLLAGEN.
 FACTOR AND CLUGGE.

-! SIMILARIY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINIEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
PIR; 143019; 143019.
HSRP: P17494; 1KST.
PROSITE; PS00427; DISINIEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ANHESION; VENOM.
SO 52 CELL ATTACHMENT SITE (POTENTIAL).
STIE 50 52
STIE 72 AA; 7704 MW; 4B255615 CRC32;
 SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN ANTAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.
 Gaps
 Gaps
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DISINTEGRIN LUTOSIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
CROTALUS VIRIDIS LUTOSUS (GREAT BASIN RATLESNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
CROTALUS BASILICUS (MEXICAN WEST-COAST RATTLESNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
 ö
 ö
 PROSTTE; PS00427; DISINTECRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
SITE 51 53 CELL ATTACHMENT SITE (POTENTIAL)
SEQUENCE 73 AA; 7652 MW; FIAD2285 CRC32;
 1; Indels
 1; Indels
 DB 1; Length 72;
1.41e+00;
 Length 73;
 Score 6; DB 1; Le
Pred. No. 1.41e+00;
0; Mismatches 1
 Score 6; DB 1;
Pred. No. 1.41e+(
0; Mismatches
 73 AA.
 PRT;
 9.4%;
larity 85.7%;
Conservative
 / Match 9.4%;
Local Similarity 85.7%;
 6; Conservative
 STANDARD;
 Local Similarity
```

```
MEDLINE; 93123215.

RA SCARBOROUGH R.M., ROSE J.W., NAUGHTON M.A., PHILLIPS D.R.,

RA SCARBOROUGH R.M., CAMPBELL A.M., CHARO I.F.;

A BIOL. CHEM. 268:1058-1065(1993).

C. -! FUNCTION: INHEBETS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS

CC GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND

CC INHEBITS AGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING

CC GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND

CC INHEBITS AGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING

FACTOR AND COLLAGEN

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF GPIIB-IIIA PROTEIN

ANTRAGONISTS, CALLED DISINTEGRINS, WHICH ARE FOUND IN SNAKE VENOM.

R SESP; P17494; IKST.

PROSITE; PS00427; DISINTEGRINS; 1.

PROSITE; PS00427; DISINTEGRINS; 1.

R BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.

FT SITE

SCELL ATTACHMENT SITE (POTENTIAL).
 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DISINTEGRIN LACHESIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).
LACHESIS MUTA MUTA (BUSHMASTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
 Score 6; DB 1; Length 73;
Pred. No. 1.41e+00;
0; Mismatches 1; Indel
73 AA.
 PRT;
 Query Match 9.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
 STANDARD;
DISI_LACMU
P31990;
 SEQUENCE
 S F S
```

Search completed: Fri Sep 25 13:22:39 1998 Job time: 7 secs.

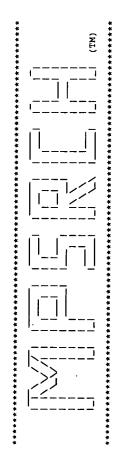
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Gaps

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1; Indels



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protein - protein database search, using Smith-Waterman algorithm srch\_pp

Fri Sep 25 13:13:59 1998; MasPar time 8.31 Seconds 7.791 Million cell updates/sec Run on:

Tabular output not generated

(1-4) from PCTUS9816719A.pep 32 >PCT-US98-16719-14 Description: Perfect Score: Sequence:

1 MLDG 4

131922 seqs, 16180660 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part29 a-geneseq32

Mean 12.453; Variance 30.777; scale 0.405 tatistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result<br>No. | Score | %<br>Ouery<br>Match | %<br>Duery<br>Match Length DB | DB | Ð      | Description            | Pred. No. |
|---------------|-------|---------------------|-------------------------------|----|--------|------------------------|-----------|
|               | 32    | 100.0               | 15                            | 15 | R83281 | HIV principal neutral  | 5.330+02  |
| 7             | 32    | 100.0               | 20                            | 12 | R75665 | Human plastin N-termi  | 5.33e+02  |
| e             | 32    | 100.0               | 21                            | ព  | R54211 | N-terminal fragment o  | 5.33e+02  |
| 4             | 32    | 100.0               | 47                            | œ  | R41943 | Serotonin receptor 5-  | 5.33e+02  |
| S             | 32    | 100.0               | 73                            | 16 | R81408 | Hepatitis GB virus (H  | 5.33e+02  |
| 9             | 32    | 100.0               | 90                            | Н  | P82591 | ORF3 protein from Bac  | 5.33e+02  |
| 7             | 32    | 100.0               | 161                           | 27 | W34524 | hTCP161 protein.       | 5.33e+02  |
| œ             | 32    | 100.0               | 220                           | 16 | R92058 | Heptaprenyl diphospha  | 5.33e+02  |
| 6             | 32    | 100.0               | 261                           | m  | R13497 | P. denitrificans COB F | 5.33e+02  |
| 10            | 32    | 100.0               | 272                           | 11 | R89766 | Transcriptional silen  | 5.33e+02  |
| 11            | 32    | 100.0               | 285                           | 78 | W27711 | R.prowazekii SpaP aut  | 5.33e+02  |
| 12            | 32    | 100.0               |                               | 78 | W27713 | R. typhi SlpT autotra  | 5.33e+02  |
| 13            | 32    | 100.0               |                               | 53 | W41374 | MTOM5, modified phyto  | 5.33e+02  |
| 14            | 32    | 100.0               | 432                           | 18 | R98464 | Murine Ich-3.          | 5.33e+02  |
| 15            | 32    | 100.0               | 479                           | œ  | R41942 | Serotonin receptor 5-  | 5.33e+02  |
| 16            | 32    | 100.0               | 481                           | 22 | W40814 | Human 5-HI2B receptor  | 5.33e+02  |
| 17            | 32    | 100.0               | 521                           | m  | R12400 | Enantioselective amid  | 5.33e+02  |
| 18            | 32    | 100.0               | 521                           | 4  | R24529 | Enantioselective amid  | 5.33e+02  |

| ed by 5.33e+02    | 'n                    | 'n.                   | 5.3               | inv               | 5.3                   | 5.3                   | 5.3               | ۳.              | -                 | ۳.              | der1 5. | n tra  | del 5. | tra 5.3           |                   | e co 5.            | by A 5.3         |             | ۳.           | ۳.             | 5.3    | ٣.     | mu 5.3 | 5.3    | £ 5.33              | polypepti 5.33e+02 |
|-------------------|-----------------------|-----------------------|-------------------|-------------------|-----------------------|-----------------------|-------------------|-----------------|-------------------|-----------------|---------|--------|--------|-------------------|-------------------|--------------------|------------------|-------------|--------------|----------------|--------|--------|--------|--------|---------------------|--------------------|
| t-plastin derived | Newcastle's disease v | Haemagglutinin-neuram | Newcastle disease | snbA gene product | Asparagine synthetase | DNA encoding recombin | Recombinant furin | Human BMP proce | Recombinant furin | Tissue-plastin. |         | ombina |        | Recombinant furin | Human pro-hormone | Murine pro-hormone | Sequence encoded | Human PACE. | Human furin. | PACE composite | Furin. |        | 11lus  | _      | Peptides translated | Enteroviral pol    |
| P94045            | R80558                | R39703                | R58598            | R54205            | R07999                | W21962                | W21963            | M36099          | W21964            | R11490          | R30089  | W21959 | W21960 | W21961            | R59784            | R67764             | R37617           | R77540      | R77539       | R24461         | R11926 | R07454 | R99255 | R82067 | 0                   | R12141             |
| Н                 | 15                    | œ                     | ;                 | 2                 | ~                     | 27                    | 27                | 28              | 27                | ~               | ø       | 27     | 27     | 27                | 11                | 11                 | ^                | 15          | 12           | Ŋ              | ~      | ~      | 13     | 16     | Н                   | 7                  |
| 547               | 577                   | 577                   | 581               | 582               | 583                   | 585                   | 591               | 595             | 597               | 630             | 641     | 709    | 713    | 719               | 753               | 753                | 753              | 794         | 794          | 794            | 794    | 868    | 1307   | 1422   | 2164                | 2185               |
| 100.0             | 100.0                 | 100.0                 | 100.0             | 100.0             | 100.0                 | 100.0                 | 100.0             | 100.0           | 100.0             | 100.0           | 100.0   | 100.0  | 100.0  | 100.0             | 100.0             | 100.0              | 100.0            | 100.0       | 100.0        | 100.0          | 100.0  | 100.0  | 100.0  | 100.0  | 100.0               | 100.0              |
| 32                | 32                    | 32                    | 32                | 32                | 32                    | 32                    | 32                | 32              | 32                | 32              | 32      | 32     | 32     | 32                | 32                | 32                 | 32               | 32          | 35           | 32             | 32     | 32     | 32     | 32     | 32                  | 32                 |
| 19                | 20                    | 21                    | 22                | 23                | 24                    | 25                    | 56                | 27              | 28                | 58              | 30      | 31     | 32     | 33                | 34                | 35                 | 36               | 37          | 38           | 39             | 40     | 41     | 42     | 43     | 44                  | 45                 |

## ALIGNMENTS

Cartifaction of the property of the property of the present sequence of the conjugate, useful as a vaccine for AIDS, has the formula (SPNE)n-(OMPC), where SPNE is a selected principal neutralisation epituh, which is one of 27 specified polypeptides (including the present sequence) or their fragments containing at least 5 amino acids and including the GPGR loop region or its homologue; OMPC is purified outer membrane proteosome of Neisseria (pref. N. meningitidis); and n. is 1-200, indicating the number of SPNE molecties covalently linked to the OMPC. The conjugates may be substituted by anions, and conjugation may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly neutralising monoclonal antibody (447 antibody) in a competition assay in the presence of natural HIV antigen such as gpl20, and were originally identified in the screening of phage epitope libraries having randomly or semi-randomly generated epitope polypeptides accessible to their corresponding DNA sequence, in turn determined by PCR. Sequence 15 AA; New antigenic conjugate useful as vaccine for AIDS - comprising HIV principal neutralisation epitope covalently linked to outer membrane proteosome of Neisseria Claim 14; Page 10; 73pp; English. R83281;
25-APR-1996 (first entry)
E HTV principal neutralisation epitope binding to 447 antibody.
E HTV principal neutralisation epitope; vaccine; HIV;
SPNE: selected principal neutralisation epitope; vaccine; HIV;
outer membrane proteosome; Neisseria; OMPC; AIDS; 447 antibody.
Synthetic.
N GB2282378-A.
D G5-APR-1995.
F 23-SEP-1994; 019253.
F 30-SEP-1994; 019253.
A (MERI ) MERCK & CO INC.
A (MERI ) MERCK & CO INC.
B Annold BA, Conley AJ, Keller PM, Shaw AR;
WPI: 95-125265/17. .r 1 R83281 standard; peptide; 15 AA. RESULT 

Score 32; DB 15; Length 15; Pred. No. 5.33e+02; 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100.0%;
Matches 4; Conservative

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Gaps

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usilvatives. Recombinant cells may also be used for the bioconversion of streptogramins from one form to another or for the production of hybrid antibiotics. Sequence 21 AA;
 5-Hydroxy-tryptamine receptor - used to identify drugs with receptor activity bisclosure; page 16; 20pp; English.

The plasmid PHD5HT2f comprises the sequence 049781 which codes for novel serotonin receptor. Fragments of the full-length coding region are disclosed as suitable for use as probes to find homologous (receptor) sequences. The preferred fragments are those coding for the G-Loop, the N-terminal and the C-terminal of the 5-HT2f receptor (R41943-R41945, respectively).
 10-MAY-1994 (first entry)
Serotonin receptor 5-HT2f G-loop region.
5-hydroxytryptamine; receptor; serotoninergic; vasoconstriction;
plasmid pHD5HT2f; G-loop; probe.
 Score 32; DB 10; Length 41;
Pred. No. 5.33e+02;
...aa+ches 0; Indels
 Score 32; DB 8; Length 47;
Pred. No. 5.33e+02;
0; Mismatches 0; Indels
 02-JUL-1996 (first entry)
Hepatitis GB virus (HGBV) clone 4 protein prod.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
 /note= "corresponding codon STOP codon"
 /note= "corresponding codon STOP codon"
 /note= "corresponding codon STOP codon"
 reagents; non-A; non-B; non-C; non-D; non-E; clone 4; tamarin; infected plasma; lambda phage; cDNA library.
 note= "corresponding codon STOP
 Location/Qualifiers
 R81408 standard; Protein; 73 AA.
 LT 4
R41943 standard; Protein; 47 AA.
R41943;
 Match 100.0%;
Local Similarity 100.0%;
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 Conservative
 : US-196030.
: US-242654.
: US-283314.
 07-APR-1993; 302759.
09-APR-1992; US-864005.
 (ELIL) LILLY & CO ELI.
Baez M, Kursar JD;
 tamarin; infected p
Hepatitis GB virus
 WPI; 93-322574/41.
N-PSDB; Q49782.
 misc_difference 20
 misc_difference 46
 misc_difference 63
 misc_difference 68
 17-AUG-1995.
14-FEB-1995; U
 13-MAY-1994;
29-JUL-1994;
 WO9521922-A2
 44 mldg 47
 |||||
| MLDG 4
 1 mldg 4
 1 MLDG 4
 Sequence
 Query Match
 Baez M,
 R81408;
 Best Loca
Matches
 RESULT RE
 RESULT
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 This is the proper and an antibiotic biosynthesis - for produce or bio-conversion of streptogramin(s) or produced in the product of streptogramin(s) or produced or streptogramin intermediates, derive, or hybrid antibiotics brample 5.2.2; Page 24; B3pp: French.

This is the N-terminal sequence of the snaA gene product and was the sisted to synthesise a degenerate probe. The snaA gene product is involved in the biosynthesis of streptogramins, antibiotics active against Gram-positive bacteria. The identification of the sequences encoding the enzymes involved in the biosynthetic pathway or means that they can be isolated and manipulated. Mutant microoraganisms in which a step in the streptogramin biosynthetic pathway is blocked can be cultured to produce streptogramin in the micromediates, which may later be converted to streptogramin
 Human plastin N-terminal partial peptide.
Human plastin; haemopoletic cells; neoplastic; anti-plastin antibodies.
 Gaps
 O1-NOV-1994.

P 07-JUN-1988; 203434.

R 07-JUN-1988; 103-203434.

R 16-MAR-1990; US-495256.

R 10-JAN-1991; US-4621983.

R 10-JAN-1991; US-462198.

R 10-JAN-1991; US-46219.

R 10-JAN-1
 28-NOV-1994 (first entry)
N-terminal fragment of snaA gene product.
Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme; biosynthetic pathway; Streptomyces pristinaespiralis.
Streptomyces pristinaespiralis.
 ó
 Score 32; DB 12; Length 20;
Pred. No. 5.33e+02;
0; Mismatches 0; Indels
 Lacroix P;
 25-SEP-1992; 011441.
25-SEP-1992; FR-011441.
BIRDN) RHONE POULENC RORER SA.
BIANC V, BLANCHE F, CROUZEL J, Jacques N,
Thibaut D, Zagorec M;
WPI: 94-12286/16.
 r 2
R75665 standard; Peptide; 20 AA.
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 (first entry)
 20 AA;
 Homo sapiens.
US5360715-A.
 |||||
| MLDG 4
 11-JUL-1995
 1 mldg 4
 01-APR-1994
 Seguence
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RESULT

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Gaps

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Human TCP gene nucleic acids - encoding dibasic amino acid

This sequence are polypeptide(s)

This sequence represents hrCPf61, which is encoded by a fragment of the comprises a dibasic amino acid processing endoprotease gene hhrCP and comprises a dibasic amino acid processing endoprotease gene hhrCP and comprises a dibasic amino acid processing endoprotease gene hhrCP and concleic acid molecules comprising fragments thereof that encode a dibasic amino acid processing endoprotease having proteolytic activity. The DNA of the invention encodes a protein capable of cleaving a precursor envelope protein of a virus that infects a cell expressing a CD4+ cell marker on the surface of the cell, especially where the virus is selected from a lentivirus or lymphotropic virus capable of infecting humans, apes, cats, dogs, cattle, horses, swine, sheep or monkeys. The protein encoded by nhTCP is used to identify an inhibitory compound that reduces the infectivity of an infectious agent susceptible to inhibition of Sequence 161 AA;
 Dibasic amino acid processing endoprotease gene; nhTCP; human; virus; endoprotease; proteolytic activity; precursor envelope protein cleavage; CD4+ cell surface marker; lentivirus; lymphotropic virus; infection inhibitor.
 Bacillus stearchtermophilus ATCC 10149 heptaprenyl diphosphate synthetase (HDS) is expressed by 3 open reading frames, ORFI (716152), ORFII (716152), that respectively code for 3 peptides (R92058-60). The ORFII (716154), that respectively code for 3 peptides (R92058-60). The ORFII and ORFII or ORFI, ORFII and ORFII or ORFI, ORFII and ORFII or ORFI, ORFII and Lansformed host cells, pref. Escherichia coll. They are used to produce heptaprenyl diphosphate, a blosynthetic intermediate of
 N-PSDB; T16152.
New isolated hepta:prenyl di:phosphate synthase peptide(s) - prepd.
using DNA obtd. from Bacillus stearothermophilus, useful for prepn.
 Heptaprenyl diphosphate synthetase ORFI product. Heptaprenyl diphosphate synthetase; HDS; isoprenold. Bacillus stearothermophilus strain ATCC 10149. EP-699761-A2.
 Score 32; DB 27; Pred. No. 5.33e+02; 0; Mismatches 0
 Ogura K;
 Score 32;
 of isoprenoid cpds.
Claim 1; Page 9-10; 33pp; English.
 soprenoids such as prenylquinone.
 .m. 8
82008 standard; Protein; 220 AA.
R92058;
15-MAY-1996 (first entry)
 25-NOV-1997.

05-JAN-1995; 368852.

05-JAN-1995; US-368852.

07-JUL-1993; US-088322.

15-NOV-1994; US-340185.

(UTE) UNIV ECHNOLOGY CORP.

Franzusoff A, Miranda LR;

WPI; 98-017639/02.
 Obata S,
 100.08;
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 06-MAR-1996.
26-JUL-1995; 111764.
29-JUL-1994; JP-179336.
(TOYT) TOYOTA JIDOSHA KK.
 (first entry)
 Koike A, Koyama T,
WPI; 96-130771/14.
 N-PSDB; T99061
 Homo sapiens.
 16 mldg 19
 US5691183-A.
 1 MLDG 4
 Sequence
 Query Match
 RESULT
 g
 à
 P82591;
06-NOV-1990 (first entry)
06-NOV-1990 (first entry)
08F3 protein from Bacillus phage phi 105, regulation part ofimmE region.
OPETS protein; promoter;
repressor protein; ss.
Bacteriophage phi 105.
Fromtion/Qualifiers
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 ö
 Operator DNA from Bacillus subtills phage phi 105 - used for regulating expression of structural genes in prokaryotic and eukaryotic cells
 Gaps
 Gaps
 Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus
Example 5; Pages 195-196; 661pp; English.
Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV
 The presence of repressor protein phi 105 stimulates transcription from PM and represses PR 1.e. ORF3. Sequence 90 AA;
 infected tamarin plasma, using standard procedures, was used to prepare a lambda phage HGBV CDNA library. The CDNA clone T00041, which encodes the proteins R81405-10 (the 6 possible reading frames), was rescued from the lambda phage, searched against a sequence database and found to be an unique HGBV sequence. Reagents which comprise the HGBV DNA, or its protein prods, can be used for the diagnosis, therapy or in a vaccine to prevent
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 Leary TP;
Schlauder GG;
 Length 73;
 Score 32; DB 16; Length 73;
Pred. No. 5.33e+02;
0; Mismatches 0; Indels
 Score 32; DB 1; Length 90;
Pred. No. 5.33e+02;
0; Mismatches 0; Indels
 21..40 /label-putative DNA binding domain
 Buijk SL, Dawson GJ, Desai SM, Erker JC, L
Muerhoff AS, Mushahwar IK, Pilot-Matias TJ,
 W34524 standard; Protein; 161 AA.
 P82591 standard; protein; 90 AA.
 Match 100.0%;
Local Similarity 100.0%;
es 4; Conservative
 Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 W34524;
24 WAR-1998 (first entry)
hTCP161 protein.
23-NOV-1994; US-344190.
23-NOV-1994; US-344185.
27-JAN-1995; US-344557.
(ABBO) ABBOTT LAB.
Buljk SL, Dawson GJ, De
 05-OCT-1988.
29-MAR-1988; 200591.
30-MAR-1987; NL-000740.
 Disclosure; p; English.
 (SOLV) SOLVAY & CIE.
 88-280012/40.
 95-293123/38.
 73 AA;
 N-PSDB; T00041.
 HGBV infection.
 organisms.
 N-PSDB; N81167
 64 mldg 67
 EP-285220-A.
 1 MLDG 4
 1 mldg 4
 1 MLDG 4
 Simons JN;
 Sequence
 Dhaese P;
 Query Match
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RESULT PRESULT 
Matches

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0; Indels

Length 161;

DB 16; Length 220;

RESULT ID W3 AC W3 DT 24 DE hT

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224 mldg 227
 1 MLDG 4
 5-SEP-1997
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Sequence
 Sequence
 Query Match
 protein.
 Protein
 Best Loca
Matches
 Matches
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 cobalamin, esp. coenzyme B12 prodn.

Claim 17; Fig 16; 299pp; French.

This sequence corresponds to one of 24 polypeptides obtained from P.dentrificans and implicated in the biosynthesis of cobalamines and/or cobamides, specifically in catalysing the transfer of a methyl group to positions Cl, C5, C11, C15 or C17 in the conversion of precorrin-3 to cobyrnic acid a, c.-diamide. It is encoded by part of the B.7kb EcoRI-EcoRI fragment of plasmid pX1367. The plasmid was isolated from a P.denitrificans genomic DNA bank constructed in
 Gaps
 Tet repressor; Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
 Gaps
 New tetracycline-regulated transcription modulators - comprising fusion proteins which bind to tet operator sequences to activate or
 ö
 ö
 New polypeptide(s) involved in cobalamin and cobamide biosynthesis - and DNA encoding them, for amplification of
 Length 261;
 0; Indels
 Indels
 (RHON) RHOWE-POULENC BIOCH.
Blanche F, Meron B, Crouzet J, Debussche L, Levy-Schil
 07-JUL-1996 (first entry)
Transcriptional silencer domain of the v-erbA oncogene.
 25-ocT-1991 (first entry)
Pofenitrificans COB F.
cob gene; corrinoid; descobaltocorrinoid; cor gene.
Pseudomonas denitrificans.
Pred. No. 5.33e+02;
 Score 32; DB 3; Le
Pred. No. 5.33e+02;
0; Mismatches 0;
 0; Mismatches
 inhibit transcription
Claim 46; Page 83-84; 112pp; English
 .r 9
R13497 standard; Protein; 261 AA.
 T 10
R89766 standard; Protein; 272 AA.
 Best Local Similarity 100.0%;
Matches 4; Conservative
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 08-AUG-1991.
30-JAN-1991; F00054.
31-JAN-1990; FR-001137.
 01-JUL-1994; US-270637.
15-JUL-1994; US-275876.
03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
 Bujard H, Gossen M;
WPI; 96-087666/09.
 29-JUN-1995; U08179
 vector pXL59.
See Q13284-Q13288.
Sequence 261 AA;
 WPI; 91-252650/34.
 (BUJA/) BUJARD H.
(GOSS/) GOSSEN M.
 N-PSDB; T11354
 transcription.
 N-PSDB; Q1328
 191 mldg 194
 WO9601313-A1.
 Homo sapiens
 1 MLDG 4
 1 mldg 4
 1 MLDG 4
 18-JAN-1996
 Thibaut D;
 RESULT
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This sequence represents an autotransporter membrane integration region from the R. prowazekii SpaP protein. This region is involved in a novel method which allows the presentation of stable fusion polypeptides on the C surface of Gram-negative bacteria which can be released into the surface of gram-negative bacteria which can be released into the c surrounding media. The method can be used to produce a variegated completion of surface-presented polypeptides, so that bacteria expressing polypeptides with particular properties can be identified and simultaneously selected, e.g. for epitope mapping or selection of ligands with the highest affinity for antibodies, major histocompatibility complex (MHC) molecules or other components of the immune system.

Selected polypeptides can be used diagnostically, e.g. to screen sera or antibody banks, and polypeptide expressing cells may be used as live c vaccines. They may be used therapeutically, e.g. when the polypeptide is an antibody, to remove or concentrate pollutants, inactivate toxins, c prepare and process food, prepare washing compositions and label cells.

Selected bacteria can be stored, reproduced and replicated on a large
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Fusion proteins comprising a first polypeptide which binds to a tet operator sequence in the presence of tetracycline or a tetracycline analogue, operatively linked to a second polypeptide which either activates or inhibit transcription in eukaryotic cells may be used to activate or inhibit transcription. Such proteins may be used to regulate gene expression in cells and may be particularly useful for organisms. Induction of gene expression of gene products in transgenic organisms. Induction of gene expression is rapid, efficient and strong, typically 1000-2000 fold. The inducing agent does not cause pleitropic effects or cytotoxicity in eukaryotic cells. This sequence encodes the transcriptional silencer domain of the v-erbA oncogene product which is used in a transcription inhibiting fusion
 Gaps
 Gaps
 via transformation with vector encoding signal peptide, presented peptide and transporter domain of auto-transporter, producing peptide libraries for epitope mapping
 Presentation of peptide(s) on surface of Gram-negative bacteria
 R. prowazekii Spap autotransporter membrane integration region. Spap protein; autotransporter; diagnostic; therapy; Gram-negative bacteria; surface presented polypeptide.
 ö
 ö
 Length 272;
 Length 285;
 Indels
 0; Indels
 Score 32; DB 28; Lew
Pred. No. 5.33e+02;
 /note= "partial protein sequence"
 (PLAC.) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN JOSE J, MAURER J, Meyer TF; WPI; 97-480227/44.
 Score 32; DB 17;
Pred. No. 5.33e+02;
 0; Mismatches
 Location/Qualifiers
 W27711 standard; Protein; 285 AA
 Claim 8; Fig 15; 84pp; German.
 Match 100.0%;
Local Similarity 100.0%;
es 4; Conservative
 Query Match
Best Local Similarity 100.0%;
 08-MAY-1998 (first entry)
 4; Conservative
 15-MAR-1996; E01130.
15-MAR-1996; WO-E01130.
 Rickettsia prowazekii
 272 AA;
 WO9735022-A1.
 79 mldg 82
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1 MLDG

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Presentation of peptide(s) on surface of Gram-negative bacteria - via transformation with vector encoding signal peptide, presented PT via transformation with vector encoding signal peptide, presented PT peptide and transporter domain of auto-transporter, producing peptide and transporter domain of auto-transporter membrane integration region This sequence represents an autotransporter membrane integration region from the R. typhi SIPT gene. This region is involved in a novel method which allows the presentation of stable fusion polypeptides on the surface of Gram-negative bacteria which can be released into the surface of Gram-negative bacteria which can be released into the surface of Gram-negative bacteria which can be released into the surface of Gram-negative bacteria which can be identified and polypeptides with particular properties can be identified and complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

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Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other components of the immune system.

Complex (MHC) molecules or other
 ö
 MTOM5, modified phytoene synthase.
MTOM5; phytoene synthase; chloroplast targeting sequence; enzyme; tomate
protein expression enhancement; transgenic plant; carotenoid synthesis;
 N-PSDB; V17247.
Enhancing gene expression without or with reduced co-suppression
 ö
 08-MAY-1998 (first entry)
R. typhi SlpT autotransporter membrane integration region.
SltP protein; autotransporter; diagnostic; therapy;
Gram-negative bacteria; surface presented polypeptide.
 Length 285;
 Score 32; DB 28; Length 285
Pred. No. 5.33e+02;
0; Mismatches 0; Indels
 25-SEP-1997.
15-WAR-1996; E01130.
15-WAR-1996; WO-E01130.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 /note- "partial protein sequence
 Location/Qualifiers
 W41374 standard; Protein; 402 AA. W41374;
W27713 standard; Protein; 285 AA.
 11-DEC-1997.
23-MAY-1997; G01414.
07-JUN-1996; G8B-011981.
(ZENE) ZENECA LTD.
BICH CR, DTARE CR, SCHUCH WW;
WPI: 98-042198/04.
 Jose J, Maurer J, Meyer TF;
WPI; 97-480227/44.
N-PSDB; T88150.
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 (first entry)
 Lycopersicon esculentum.
 Rickettsia typhi
 224 mldg 227
 1 MLDG 4
 28-MAY-1998
 Lycopene.
 Protein
 8
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Disclosure; Page 19-21; 32pp; English.

Disclosure: Page 19-21; 32pp; English.

This sequence represents the modified phytoene synthase MTOMS, which this sequence represents the modified phytoene synthase MTOMS, which can calcorplast targeting sequence. The MTOMS gene is used in the method of the invention for enhancing expression of a protein by an organism, comprising inserting into its genome a nucleotide sequence of produces different RNA on transcription to that of the gene already present, but produces the same protein on translation. Transgenic plants with enhanced ability to express a selected can be produced by the compact for for example, the method can be used to achieve overexpression of a gene specifying an enzyme necessary for carotenoid synthesis in plants (especially phytoene synthase), to enhance carotenoid expression of colouration of developing tomato fruit. Protein expression is enhanced by colouration agene construct which is altered by maximising the caroteded protein. Known methods of increasing protein production by gene concoded protein. Known methods of increasing protein production by gene concoded protein. Rnown methods of increasing protein production by gene capecially when the recombinant and endogenous gene sequences are similar. The method allows enhanced expression whilst avoiding or reducing co-suppression, since sequence similarity between the two genes formed.
 cell
 other related genes
Claim 24: Fig 14: 127pp; English.
Ich-3 (R98464) causes programmed cell death and shows significant
homology to mouse interleuth-1 beta converting enzyme (ICE),
mouse mIch-2 (R98461) and human Ich-1 (R98462-63). Its sequence
was deduced from the Ich-3 gene (731554) isolated from a mouse thymus
cDNA library. The protein can be obted. from host cells contg.
vectors that include an Ich-3 coding sequence. It can be used to
control the programmed cell death of vertebrate cells, to develop cell
lines that remain viable for extended periods, and to increase the
using altered DNA producing different RNA but same protein as natural gene, useful especially in plants to allow overexpression of a protein
 Gaps
 Gaps
 Preventing or promoting programmed cell death in vertebrate cells comprises inhibiting or increasing the activity of interleukin-1-beta converting enzyme, or altering expression of
 ICh-3; murine ICE-ced-3 homologue; programmed cell death; apoptosis; interleukin-1 beta converting enzyme; gene therapy.
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 Score 32; DB 18; Length 432;
Pred. No. 5.33e+02;
 Length 402;
 0; Indels
 0; Indels
 Score 32; DB 29; I
Pred. No. 5.33e+02;
0; Mismatches 0;
 0; Mismatches
 T 14
R98464 standard; Protein; 432 AA.
R98464;
 04-JAN-1996; U00177.
04-JAN-1995; US-368704.
(GEM) GEN HOSPITAL CORP.
Milla M, Yuan J;
WPI; 96-333763/33.
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
 Match 100.0%;
Local Similarity 100.0%;
les 4; Conservative
 25-SEP-1996 (first entry)
 432 AA;
 N-PSDB; T31554.
 WO9620721-A1.
 195 mldg 198
 Murine Ich-3.
 36 mldg 39
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RESULT 15
R41942 standard; Protein; 479 AA.
R41942 standard; Protein; 479 AA.
AC R41942.
AC R41942.
AC R41942.
AC R41942.
BAC R41942.
BE Serotonin receptor 5-HT2f.
BW 5-hydroxytryptamine; receptor; serotoninergic; vasoconstriction;
BW 5-hydroxytryptamine; receptor; serotoninergic; vasoconstriction;
BW 5-hydroxytryptamine; receptor; serotoninergic; vasoconstriction;
BW 5-56370-A.
BW 6-56370-A.
BW 6-56370-A.
BW 6-7-1993; 302759.
BW 6-1993; 302759.
BW 6-1993; 302759.
BW 7-1993; 302759.
BW 8-1993; 302759.
BW 8-1993; 302759.
BW 9-1993; 302759.

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Search completed: Fri Sep 25 13:14:12 1998 Job time : 13 secs.

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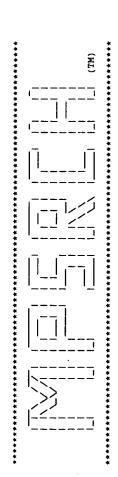
Gaps

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Query Match 100.0%; Score 32; DB 8; Length 479; Best Local Similarity 100.0%; Pred. No. 5.33e+02; Matches 4; Conservative 0; Mismatches 0; Indels

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Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Sep 25 13:12:59 1998; MasPar time 5.67 Seconds 29.730 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-14 (1-4) from PCTUS9816719A.pep 32 1 MLDG 4 Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

140555 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified sptremb16

Mean 17.810; Variance 17.293; scale 1.030 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Duery Match Length DB ID
0 261 11 083473
100.0 437 11 036416
100.0 448 12 099293
100.0 455 11 Q8551
100.0 460 11 Q82115
460 11 (
100.0 462 11 Q84804
473 12 (
521 12
100.0 577 11
577 11 (
577 11
.00.0 582 11
0 595 12

3.02e+02 3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02	3.02e+02 3.02e+02 3.02e+02 3.02e+02 3.02e+02
DNA POLYMERASE (FRAGME PC7B (FRAGMENT). POLYPROTEIN (FRAGMENT) ENDOPEPTIDASE PC1.	TRANS GOLGI NETWORK PR COMPLEMENT REGULATORY METHIONINE SYNTHASE. 1.1-1.TRE CELL. ADHESTON	STRUCTURAL POLYPROTEIN NEUROFASCIN PRECURSOR. CALCIUM TRANSPORTING A	NEUROFASCIN PRECURSOR. COUNTERPART OF HSV-1 G DNA TOPOISOMERASEII_BE		CVB3 POLYPROTEIN. POLYPROTEIN. POLYPROTEIN.	COMPLETE GENOME. ECHOVIRUS TYPE 12, PRO ECHOVIRUS TYPE 12, PRO ECHO VIRUS 11 GENOMIC POLYPROTEIN.
038017 Q63794 Q66473 Q91065	Q91000 Q91275 Q33259	P89946 Q90924 Q36028	042414 039283 042131	Q82122 Q86887 Q88445	Q66282 Q66338 Q66474	Q66849 Q66576 Q66575 Q66785
110	1367	1121	1112	111	111	=== ===
621 631 665 775	789 1053 1192	1239 1272 1367	1369 1375 1627	2153 2183 2185	2185 2185 2191	2193 2193 2193 2195 2203
100.0 100.0 100.0	0.000	100.0	100.0 100.0 100.0	100.0 100.0 100.0	100.0	1000.00
3322	2222	3523	333	332	322	33333
23 23 24		330	333 34 34	35 36 37		4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALCELAPHINE HERPESVIRUS 1 (WILDEBEEST HERPESVIRUS).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                          Score 32; DB 11; Length 261; Pred. No. 3.02e+02; 0; Mismatches 0; Indels
                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
COAT PROTEIN.
SOUTHERN BEAN WOSALC VIRUS (SBMV).
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; SOBEMOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                               11 2 2 PRELIMINARY; PRT; 437 AA. 036416; 036416; 01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) 0RF66.
                                                                                                                                                                                                                                                             261 AA; 28106 MW; 91032C8A CRC32;
               261 AA
                                                                                                                                                                       MEDLINE; 95133162.

OTHMAN Y., HULL R.;
VIROLOGY 206:287-297(1995).

EMBL; L34672; G511649; -

PROSITE; PS00555; ICOSAH_VIR_COAT_S; 1.

COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C500;
ENSSER A., PFLANZ R., FLECKENSTEIN B.;
J. VIROL. 71:6517-6525(1997).
               PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BEAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     229 MLDG 232
                                                                                                                                                                                                                                                                                                                                                                       1 MLDG 4
                                                                                                                                                                                                                                                                SEQUENCE
LT 1
Q83473
Q83473;
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
11D 03
AC 03
DT 011
DT 011
DT 02
NT 011
RP NT [1]
RR SE ST
RR EN C ST
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Gaps

LT 3 Q99293 Q99293;

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RESULT

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04804
084804
084804
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
03D PROTEIN.
03D PROTEIN.
04D PROSICULAR DISEASE VIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICCRNAVIRIDAE; ENTEROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
MEDLINE; 87204179.
MEDLINE; 87204179.
DUECHLER M., SKERN T., SOMMERGRUBER W., NEUBAUER C., GRUENDLER P., FOGY I., BLAAS D., KUECHLER E.;
PROC. NATL. ACAD. SCI. U.S.A. 84:2605-2609(1987).
EMBL; M16248; E3570; ...
                                                                                                                                                                                                                                                                                                                                                                     HUMAN RHINOVIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; ISOMETRIC SS-RNA VIRUSES;
PICORNAVIRIDAE; RHINOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN RHINOVIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; ISOMETRIC SS-RNA VIRUSES;
PICORNAVIRIDAE; RHINOVIRUS.
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
Indels
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SEQUENCE FROM N.A.
MEDLINE; 8089537.
HUGHES P.J., NORTH C., JELLIS C.H., MINOR P.D., STANWAY Of GEN VIROL. 69:49-58(1988).
EMBL; D00239; E19866; -.
SEOUENCE 460 AA; 52327 MW; 3F963020 CRC32;
                                                                                                                                                                                                                                                   UL-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
POLYMERASE.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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0; Mismatches
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
POLYMERASE.
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Local Similarity 100.0%;
nes 4; Conservative
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Best Local Similarity 100.0%;
Matches 4; Conservative
4; Conservative
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SEQUENCE FROM N.A.
                                                 245 MLDG 248
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AC 082115
AC 082115
DT 01-NOV-1996 (7
DT 01-NOV-1996 (7
DT 01-NOV-1996 (7
DE POLYMERASE.
OS HUMAN RHINOVI
CC VIRIDAE; SS-R
OC PICCENAVIRIDA
RN [1]
RP SEQUENCE FROM
RX MEDLINE; 8808
RA HUGHES P.J.,
RL J. CEN. VIROLL
DR EMBL; DO0239;
SQ SEQUENCE 456
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                                                                                   1 MLDG 4
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Q82105
Q82105;
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Matches
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EURARXOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
POLYPROTEIN GAG-P75-ERBA (FRAGMENT).
AVIAN ERYTHROBLASTOSIS VIRUS.
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
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DEBUINE; 84223957.
DEBUINE B., HENRY C., BENAISSA M., BISERTE G., CLAVERIE J.M., SAULE S., MARTIN P., STEHELIN D.; SCIENCE 224:1456-1459(1984).
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL. KOZOGG; G209662; -.
PROSITE: PSO0031; NUCLEAR_RECEPTOR; 1.
POLYPROTEIN; RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 11; Length 455; Pred. No. 3.02e+02;
                                                                                                                                                                                      Length 437;
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
                                                                                                                                                                              Score 32; DB 11; Length 437
Pred. No. 3.02e+02;
0; Mismatches 0; Indels
                STRAIN-C500;
ENSSER A., PFLANZ R., FLECKENSTEIN B.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF005370; G2338029; -.
SEQUENCE 437 AA; 49383 MW; A37BC311 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
OCTAMER-BINDING TRANSCRIPTION FACTOR 25 (OCT-25)
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01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-FEB-1997 (TREMBLREL. 02, LAST ANN
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SEQUENCE FROM N.A.
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             PRT;
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             PRELIMINARY;
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Best Local Similarity 100.0%;
Matches 4; Conservative
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01-MAY-1997 (TREMBLREL.
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Q96594
Q96594;
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01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
61-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
6ABAC RECEPTOR SUBURT RHO-1B.
MORONE AMERICANA (WHITE PERCH).
EUKARYOTAE: MITOCHONDRIAL EUKARYOTES; METAZOA; CHORDATA; VERTEBRATA;
ACTINOPPERKGII; NEOPTERKGII; TELEBOSTEI; EUTELEOSTEI; ACANTHOPTERYGII;
PERCOMORPHA; PERCIFORMES; PERCOIDEI; MORONIDAE; MORONE.
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QIAN H., HYATT G., SCHANZER A., HAZRA R., HACKAM A., CUTTING G.R.,
DOWLING J.E.;
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
                                                                                                                                                                    Length 462;
                                                                                                                                                              Score 32; DB 11; Length 462
Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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MEDLINE; 90364770.
SEECHURN P., KNOWLES N.J., MCCAULEY J.W.;
VIRUS RES. 16:255-274(1990).
SEDUENCE 462 As; 52527 MW; 04697EA2 CRC32;
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STALHANDSKE P.O.K., LINDBERG M., PETTERSSON U.
J. VIROL. 51:742-746(1984).
POLYPROTEIN.
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EMBL: AF010287; G2317700; -.
SEQUENCE 473 AA; 54396 MW; 60C7B97B CRC32;
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nes 4; Conservative
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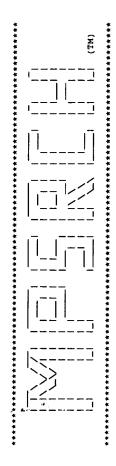
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
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01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREAGRENT)
01-JAN
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01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSPORMATION-DEFECTIVE NUTRANT TD359 PROVIRAL GAG (3' END), ERBA
AVIAN ERYTHROBLASTOSIS VIRUS.
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EMBO J. 6:375-382(1987).
-- SUBCELLUAR LOCATION: NUCLEAR (BY SIMILARITY).
-- PROSITE; M32090; G209565; --
PROSITE; PS00031, NUCLEAR_RECEPTOR; 1.
POLYPROTEIN; RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
NUCLEAR PROTEIN; 21NC-FINGER.
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CHAIN 1 171 POTENTIAL.
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VXAZAKI K., HAYASHIDA K., IWASHITA J., HARANO M., FURUNO 1
SAGATA N.;
GENE 178:111-114(1996).
EMBL; D82960; G1777328; -.
SEQUENCE 521 AA; 59911 MW; BAIE8D33 CRC32;
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
03, CREATED)
03, LAST SEQUENCE UPDATE)
03, LAST ANNOTATION UPDATE)
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555 AA; 61660 MW; 48B1789A CRC32;
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491 MLDG 494
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NEWGASTLE DISEASE VIRUS (NDV).
VIRIDAE: SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; PARAMYXOVIRIDAE;
PARAMYXOVIRUSES.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
101-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
NEWCASTLE DISEASE VIRUS (NDV).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; PARAMYXOVIRIDAE;
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VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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Pred. No. 3.02e+02;
0; Mismatches 0; Indels
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                            MEDLINE; 87218491.
DAMM K., BEUG H., GRAF T., VENNSTROEM B.;
EMBO J., 6:375-382(1987).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
                                                                                                                                                      POTENTIAL.
POTENTIAL.
9E221BDF CRC32;
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STRAIN-VACCINE 4 (LASOTA TYPE);
SEAL B.S., KING D.J., BENNETT J.D.;
VCCINE 14.761.766(1996).
EMBL; U37190; G1145274; -.
SEQUENCE 577 AA; 63231 MW; 62F451D5 CRC32;
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SEQUENCE FROM N.A.
STRAIN-B1(SEPRL);
SEAL B.S., KING D.J., BENNETT J.D.;
VACCINE 14:761-766(1996).
EMBL; U37193; G1142280; -.
SEQUENCE 577 AA; 63215 MW; 53C414
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1 170 PO
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Matches 4; Conservative
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Q83846;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
HEMAGLUTININ-NEURAMINIDASE.
NEWASATLE DISEASE VIRUS (NDV).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; PARAMYXOVIRIDAE;
PARAMYXOVIRUSES.
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SEQUENCE FROM N.A.
STRAIN-VACCINE 5 (B1 TYPE);
SEAL B.S., KING D.J., BENNETT J.D.;
VACCINE 14:761-766(1996).
EMBL; U37191, G1145276; -.
SFOUENCE 577 AA; 63409 MW; 72CEF942 CRC32;
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4; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

|Psrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Sep 25 13:13:31 1998; MasPar time 5.75 Seconds 25.414 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-14 (1-4) from PCTUS9816719A.pep 32 1 MLDG 4 Title: Description: Perfect Score: Sequence:

Scoring table:

120441 seqs, 36531193 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 17.866; Variance 18.225; scale 0.980 pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score	Ouery	Length	88	Ð	Description	Pred. No.
_	100.0	145	N	H69051	heterodisulfide reduc	3.30e+02
	100.0	174	~	A48198	voltage-dependent cal	3.30e+02
a	100.0	240	~	F65036	hypothetical protein	3.30e+02
	100.0	284	~	F70024	diaminopimelate epime	3.30e+02
	100.0		Н	OWPSAA	ornithine carbamovitr	3.30e+02
	100.0		~	G64889	hypothetical protein	3.30e+02
٠.	100.0		2	1WAIB	DNA polymerase (EC 2.	3.30e+02
٠.	100.0		ເດ	1WAIA	DNA polymerase (EC 2.	3.30e+02
	100.0		ഹ	2POLA	Pol 111 (beta subunit	3.30e+02
_	100.0		ស	2POLB	Pol 111 (beta subunit	3.30e+02
	100.0		~	S35744	transforming protein	3.30e+02
	100.0		-	ADSPAP	fructose-bisphosphate	3.30e+02
~	100.0	429	~	A47305	translation initiatio	3.30e+02
a	100.0		7	A46259	recA protein homolog	3.30e+02
~	100.0		7	A38079	gamma-aminobutyric ac	3.30e+02
~	100.0		~	A38627	gamma-aminobutyric ac	3.30e+02
~	100.0		~	S43687	serotonin receptor 5-	3.30e+02
٠.	100.0	523	~	B38145	invariant surface qly	3.30e+02
~	100.0		7	JC2468	folate transporter -	3.30e+02
2	100.0		7	B41627	furin homolog 18 - Af	3.30e+02
^	100.0		~	S62580	hypothetical protein	3.30e+02
~	100.0		~	I84634	Tamm-Horsfall protein	3.30e+02
^-	100.0	655	7	A54306	proprotein convertase	3.30e+02

100.0 710 2 B46184 prohormone-processing 3.30e+02 100.0 720 5 10ACA copper amine oxidase 3.30e+02 100.0 720 5 10ACA copper amine oxidase 3.30e+02 100.0 723 5 10ACB copper amine oxidase 3.30e+02 100.0 723 5 10ACB copper amine oxidase 3.30e+02 100.0 752 1 KKRTC1 prohormone-processing 3.30e+02 100.0 871 2 84356 Lfur2 protein homolog 3.30e+02 100.0 861 2 84376 Lfur2 protein homolog 3.30e+02 100.0 861 2 871719 replication factor C 3.30e+02 100.0 861 2 874763 replication factor C 3.30e+02 100.0 861 2 87476 methionine synthase m 3.30e+02 100.0 1135 2 846199 arbibactor complement r 3.30e+02 100.0 1135 2 845199 arbibactor complement r 3.30e+02 100.0 1135 2 84559 hypothetical protein (clon 3.30e+02 100.0 1289 2 85689 hypothetical protein 3.30e+02 100.0 1289 2 849764 SECT protein (clon 3.30e+02 100.0 1377 2 B44950 orf2 of crual-associa 3.30e+02 100.0 2157 1 GNNY89 genome polyprotein - 3.30e+02 100.0 2157 1 GNNY89 genome polyprotein - 3.30e+02 100.0 2157 1 GNNY89 enniatin synthetase - 3.30e+02 100.0 2151 2 843642	NAMENINGA ORBANDA MANERO DO O	#length 145 #molecular-weight 16448 #checksum 8326 #length 145 #molecular-weight 16448 #checksum 8326 100.0%; Score 32; DB 2; Length 145; Similarity 100.0%; Pred. No. 3.30e+02; 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 66 4 A48198 #type fragments voltage-dependent calcium channel complex type L alpha-1 chain, cardiac - human (fragments) #formal_name Homo sapiens #common_name man
22222222222222222222222222222222222222	EESULT 1 H690; ENTRY H690; TITLE Meter H600; ACCESSIONS H690; REFERENCE A690; REFERENC	#gene SUMMARY Query Match Best Local Si Matches Db 1 MLDG Qy 1 MLDG RESULT 2 ENTRY TITLE ORGANISM

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                                                                              Schultz, D.; Mikala, G.; Yatani, A.; Engle, D.B.; Iles, D.E.; Segers, B.; Sinke, R.J.; Weghuis, D.O.; Kloeckner, U.; Wakamori, M.; Wang, J.J.; Melvin, D.; Varadi, G.; Schwartz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhw, G.F. Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Muu, B.; Shao,
                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6228-6232 Cloning, Ghromosomal localization, and functional expression of the alphal subunit of the L-type voltage-dependent calcium channel from normal human heart.
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17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
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#cross-references MUID:97426617
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:X #length 240 #molecular-weight 27004 #checksum 9924
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Pred. No. 3.30e+02;
0; Mismatches 0; Indels
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Pred. No. 3.30e+02;
0; Mismatches 0; Indels
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A.; Braun, M.; Borcheur, W.; Boriss, R.; Boursier, S.;
Bolotin, A.; Borcheur, S.; Boriss, R.; Boursier, S.;
Bolotin, A.; Borcheur, S.; Broiss, R.; Boursier, S.;
Brusch, C.V.; Caldwell, S.C.; Bron, S.; Brouillet, S.;
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Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
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Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
Warsher, P.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
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Warsher, P.; Wedler, R.; Yamanoto, H.; Weitzenegger, T.;
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                         ##molecule_type_DNA ##label ITO ##rosidues 1.305 ##label ITO ##rosidues 1.305 ##label ITO ##rosidues 1.305 ##label ITO ##note the authors translated the codon GAG for residues 170 ##note and 171 as Ala and ATG for residues 172 and 236 as Leu and LTO ##note carbamoyltransferase; aspartate/ornithine carbamoyltransferase homology aspartate/ornithine carbamoyltransferase homology arginine biosynthesis; homotrimer; transferase
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DNA polymerase (EC 2.7.7.7), chain B - phage rb69
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DNA polymerase from bacteriophage rb69, alpha-carbons only
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hypothetical protein b1388 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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Konigsberg, W.H.; Steitz, T.A.
#submission submitted to the Brookhaven Protein Data Bank, April 1997
#cross-references PDB:1WAI
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homology #label ACT
#length 305 #molecular-weight 34076 #checksum 9936
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#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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Resolution: not applicable
Determination: theoretical model
Complex; DNA; gp43 complex; nucleotidyltransferase; rb69 DNA
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DNA polymerase from bacteriophage rb69, alpha-carbons only
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Cell (1997) 89:1087
crystal structure of a pol alpha family replication GNA
polymerase from bacteriophage rb69.
Wang, J.; Sattar, A.K.; Wang, C.C.; Karam, J.D.; Konigsberg, W.H.; Steitz, T.A.
Cell (1997) 89:1087
                                                                                                                                                                      Wang, J.; Yu, P.; Lin, T.C.; Konigsberg, W.H.; Steitz, T.A. Blochemistry (1996) 35:8110
Crystal structures of an nh2-terminal fragment of t4 DNA polymerase and its complexes with single-stranded DNA and
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Three-dimensional structure of the beta subunit of
Escherichia coli DNA polymerase III holoenzyme: a sliding
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Cystal structures of an nh2-terminal fragment of t4 DNA polymerase and its complexes with single-stranded DNA and with divalent metal ions.
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J. Biol. Chem. (1988) 263:7478-7486
Primary structure of T4 DNA polymerase.
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Konigsberg, W.H.; Steitz, T.A.
submitted to the Brookhaven Protein Data Bank, April 1997
                                                                                                                                                                                                                                                                                                                                                  Wang, C.C.; Yeh, L.S.; Karam, J.D.
J. Biol. Chem. (1995) 270:26558
Modular organization of t4 DNA polymerase. evidence from phylogenetics.
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J. Biol. Chem. (1995) 270:26558
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expressed in Escherichia coli
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REFERENCE TN048357
#authors Wang, J.; Sat
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#submission submitted to the Brookhaven Protein Data Bank, November 1992
#cross-references PDB:2POL
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submitted to the Brookhaven Protein Data Bank, November 1992
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Call (1992) 69:425
Three-dimensional structure of the beta subunit of
escherichia coli dna polymerase iii holoenzyme: a sliding
                                              Kong, X.P.; Onrust, R.; O'Donnell, M.; Kuriyan, J. Cell (1992) 69:425-437

Three-dimensional structure of the beta subunit of Escherichia coli DNA polymerase III holoenzyme: a sliding
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Call (1992) 69.425
Three-dimensional structure of the beta subunit of
escherichia coli dna polymerase iii holoenzyme: a sliding
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#authors Spicer, E.K.; Rush, J.; Fung, C.; Reha-Krantz, L.J.; Karam, J.D.; Konigsberg, W.H.
J.D.; Konigsberg, W.H.
J. Biol. Chem. (1988) 263:7478-7486
#title Primary structure of T4 DNA polymerase.
#cross-references MUID:8827938
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Pol iii (beta subunit) (EC 2.7.7.7), chain B - Escherichia
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Modular organization of t4 DNA polymerase. evidence from
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Resolution: 2.5 angstroms
Determination: x-ray diffraction
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                 phylogenetics.
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Best Local Similarity 100.0%;
Matches 4; Conservative
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Pelzer-Reith, B.; Penger, A.; Schnarrenberger, C.
Plant Mol. Biol. (1993) 21:331-340
Plant aldolase: CDNA and deduced amino-acid sequences of the
chloroplast and cytosol enzyme from spinach.
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J. Biol. Chem. (1984) 259:1011-1017
Isolation and characterization of the cytosolic and
chloroplast forms of spinach leaf fructose diphosphate
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##cross references EMBL:X12707
FICATION #superfamily thyroid hormone receptor; erbA transforming
protein homology
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Resolution: 2.5 angstroms
Determination: X-ray diffraction
Nucleotidyltransferase
#length 366 #molecular-weight 40586 #checksum 9121
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##cross-references EMBL:X66814; NID:922632; PID:922633
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Pred. No. 3.30e+02;
0; Mismatches 0;
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#accession A21815
##molecule_type protein
##residues 47-64 ##label LEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence extracted from NCBI backbone (NCBIN:128800, NCBIP:128802) #length 429 #molecular-weight 48954 #checksum 2585
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recA protein homolog - Arabidopsis thaliana (fragment)
#formal_name Arabidopsis thaliana #common_name mouse-ear
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20-Mar-1998
A46259
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:3058-3062
Molecular cloning and expression of cDNA for mammalian
translation initiation factor 5.
                                                                                         #label TNP\
#product fructose-bisphosphate aldolase #status
    experimental #label MAT\
#active_site Lys, Lys, Tyr #status predicted
#length 393 #molecular-weight 42476 #checksum 7489
*superfamily fructose-bisphosphate aldolase
aldehyde-lyase; Calvin cycle; carbon-carbon lyase;
chloroplast; pentose phosphate pathway; tetramer
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Pred. No. 3.30e+02;
0; Mismatches 0; Indels
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##residues 1-429 ##label DAS
##cross references GB:Li1651; NID:g294544; PID:g294545
##experimental_source_insulinoma
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#cross-references MUID:92390390
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                    KEYWORDS
                                                                         1-46
                                                      FEATURE
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#authors Cutting, G.R.; Curristin, S.; Zoghbi, H.; O'Hara, B.; Seldin, M.F.; Uhl, G.R.
# Journal Genomics (1992) 12:801-806
#title Identification of a putative gamma-aminobutyric acid (GABA)
receptor subunit rho2 cDNA and colocalization of the genes encoding rho2 (GABRA2) and rho1 (GABRR1) to human chromosome 6014-921 and mouse chromosome 4.
#across-references MUID:92241882
  *superfamily recA protein
ATP; DNA binding; DNA recombination; DNA repair; SOS response
#length 438 #checksum 9097
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#predict gamma-aminobutyric acid receptor rho-2 chain
#status predicted #label MAT\
#status predicted #status predicted
#disulfide_bonds #status predicted
#length 465 #molecular-weight 54124 #checksum 5962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1.465 ##label CUT ##cross-references GB:M86868; NID:g182912; PID:g456428 ##note sequence extracted from NCBI backbone (NCBIN:99352, NCBIP:99355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Homo saplens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                             A38079 #type complete
gamma-aminobutyric acid receptor rho-2 chain precursor
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#map_position 6q14-6q21
KEYWORDS disulfide bond; neurotransmitter receptor
FEATURE
                                                                                               Score 32; DB 2; L
Pred. No. 3.30e+02;
0; Mismatches 0
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Pred. No. 3.30e+02;
0; Mismatches 0
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                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             human
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CLASSIFICATION
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

srch_pp protein . protein database search, using Smith-Waterman algorithm

Fri Sep 25 13:14:55 1998; MasPar time 4.86 Seconds 112.660 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-16 (1-13) from PCTUS9816719A.pep 107

1 CKRAMLAGLNDYC 13 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

140555 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl6
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 26.625; Variance 31.630; scale 0.842

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Statistics:

SUMMARIES

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67 62.6 63 58.9 61 57.0 60 56.1 60 56.1 60 56.1 60 56.1 60 56.1 60 60.1 60 60 60.1 60 60.1 60 60.1 60 60.1 60 60.1 60 60.1 60 60.1 60 60 60.1 60 60 60.1 60 60 60.1 60 60 60.1	Result No.	Score	Query Match	Length	80	a	Description	Pred. No.
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55 51.4 202 10 064302 1 55 51.4 225 9 044000 1 55 51.4 350 9 058993 1 55 51.4 354 9 056844 1	16	56	52.3	428	m	024024	TESTIS-SPECIFIC-RRM-PR	3.15e+00
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55 51.4 350 9 Q58993 155 51.4 354 9 Q58844	18	52	51.4	225	σ	044000	PYRUVATE DEHYDROGENASE	5.03e+00
•	19	52	51.4	350	0	058993	HYPOTHETICAL 37.8 KD P	5.03e+00
	20	55	51.4	354	σ	056844	YSCU.	5.03e+00

SEQUENCE FROM N.A. STRAIN=UW2;

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5.03e+00 5.03e+00 5.03e+00 5.03e+00 7.03e+00 7.09e+00	
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ALIGNMENTS

RESULT ID 0	Q98995 Q98995 Q98965	PRELIMINARY;	RY;	PRT;	478 AA.	i			
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5 G	UI-JAN-1998 LEBETASE LE3	(TREMBLREL. PRECURSOR.	05,	LAST ANNO	TATIO	ANNOTATION UPDATE)	a		
800	MACROVIPERA FIXARYOTAE	LEBETINA (LEVANTINE VIPER). MITOCHONDRIA: FIREARYOTES: META270a. CHODDRATA. VEDEFEDBATA.	VANT	INE VIPER	.). META	0.40	V - ATACO	0.000	400
88	LEPIDOSAURIA		SCLE	ROGLOSSA:	SERPI	NTES: C	SERPENTES: COLUBROIDEA:	EAT.	1
8	VIPERIDAE; V	VIPERIDAE: VIPERINAE: MACROVIPERA.	CROV	IPERA.				ì	
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RP	SEQUENCE FROM N.A.	OM N.A.							
ည္က	TISSUE-VENOM GLAND;	4 GLAND;							
Æ.	SIIGUR E., A		TU A	TU A.T., SIIGUR J.;	UR J.				
Z 6	BIOCHEM. BIOPHYS. RES.		OMMO	N. 224:22	9-236	1996).			
ž :	EMBL; A9/894; E246059;	1; E245059; .		,					
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FI	CHAIN	194 478		POTENTIAL					
SO	SEQUENCE 4	¥	53480 MW;	; 384418C4	-	CRC32;			
å	Query Match		e e	Score 67;	DB 12;		Length 478;		
Ma Ma	Best Local Simi Matches 7;	Similarity 53.8%; 7; Conservative	 0	Pred. No. 3; Mism	g T	-02;	Indels	ő	Gaps
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Œ	METHYLTRANSE	METHYLIRANSFERASE (MI) AND HELICASE (HEL) DOMAINS.	ND H	ELICASE (HEL) 1	NOMAINS.			
SO	LITTLE CHERF	LITTLE CHERRY CLOSTEROVIRUS.	RUS.						
႘	VIRUSES; SSF	VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CLOSTEROVIRUS	STRA	ND VIRUSE	S, NO	DNA STA	NGE; CLOS	STERO	VIRUS
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SWRE

LT 3 098810 098810;

RR RR RR RR FT FT FT SO

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A WILSON K., BURNEL M., ANDERSON K., BAYNES C., BERKS M.,
A WILSON Y., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J.,
B ONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
A COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
FULTON L., GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M.,
A JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAIGTER N.,
I.ATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
A OCALLAGABAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
SAUNDERS D., SHOWNKEN R., SMALDON N., SMITH A., SONNHAMMER E.,
A VAUGEAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
A WILKINSON-SPROAT J., WOHLDMAN P.;
LL NATURE 368:32-38(1994).

SEQUENCE 617 AA, 69269 MW; A4EC33D9 CRC32;
                                                                                                                                                                                                                                                                            BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
BULTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A.,
GOCAYNE J.D., KERLAYGE A.R., DOUGHERTY B.A., TOMB J.F.,
ADAMS M.D., REICH C.L., OVERBEEK R., KIRKNESS B.F.,
WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L.,
GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRWANN J.L., PRESIEX B.A.,
HANNA M.C., COTTON M.D., HURST M.A., ROBERTS K.M., KAINE B.P.,
HANNA M.C., COTTON M.D., HURST M.A., ROBERTS K.M., KAINE B.P.,
BORDDOVSKY M., KLENK H.P., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                            ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 3; Length 617;
Pred. No. 1.21e+00;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 9; Length 308;
Pred. No. 7.42e-01;
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01, LAST SEQUENCE UPDATE)
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EMBL; U67599; G1592202; -.
SEQUENCE 308 AA; 33442 MW; C1297C34 CRC32;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Q58986;
Q1-NOV-1996 (TREMBLREL. 0
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01-NOV-1996 (TREMBLREL. 0
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01-NOV-1996 (TREMBLREL.
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01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                      SELENIUM DONOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS
     | | | || :|| :|| | CKRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 REMLKGFQDFC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGHTNING J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VENTER J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 6
Q23332
Q23332;
                                                                                                                                                                                                           MJ1591
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                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
01-FEB-1997 (TREMBLREL.)
YAM MOSALC VIRUS.
VIRUSES, SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEGUENCE FROM N.A. SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-IVORY COAST;
ALEMAN M.E., MARCOS J.F., BRUGIDOU C., BEACHY R.N., FAUQUET C.;
ARCH. VIROL. 141:1259-1278(1996).
EMBL; U42596; G1552418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLLUSCUM CONTAGIOSUM VIRUS SUBTYPE 1 (MCVI).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI
                                                                                                          Score 63; DB 11; Length 2301;
Pred. No. 9.99e-02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61; DB 11; Length 440;
Pred. No. 2.75e-01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 11; Length 176;
Pred. No. 4.53e-01;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U60315; G1491951; -.
SEQUENCE 176 AA; 19234 MW; 19122EAC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                          EF8FDDA8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 440
440 AA; 49392 MW; F83DECBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 AA
                                                                                                                                                                                                                                                                                                 440 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TREMBLREL. 02, 01-FEB-1997 (TREMBLREL. 02, 01-FEB-1997 (TREMBLREL. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                              Query Match 58.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 56.1%;
Best Logal Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.0%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCIENCE 273:813-816(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 CGRRML-GLAQYC 44
                                                                                                                                                                                    957 RSMLMNLIEYC 967
                                                                                                                                                                                                         |:|| | :||
3 RAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 KSMLAGLRDY 208
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3 RAMLAGLNDY 12
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SEQUENCE
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LT 4 Q98179 Q98179;

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RESULT ID P7 AC P7 DT 01 DT 01 DE S1 GN YI OS EE

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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
THE RECEPTOR-ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BALTIMORE D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 10; Length 567;
Pred. No. 1.96e+00;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.3%; Score 57; DB 2; Length 543; Best Local Similarity 61.5%; Pred. No. 1.96e+00; Matches 8; Conservative 1; Mismatches 3; Indels
                                   Length 231;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                        TIŜSUE-BRAIN;
MEDLINE; 93129692.
MEDLINE; 93129692.
FEBS LETT. 358:113-118(1995).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                               Score 57; DB 9; L
Pred. No. 1.96e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 AA; 64263 MW; F85A30F3 CRC32;
0E7453D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA; 61719 MW; E9FCA764 CRC32;
                                                                 1; Mismatches
                                                                                                                                                                                                      543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L38509; G695358; -. PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                    PRT;
27143 MW;
                               53.3%;
larity 53.8%;
Conservative
                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JAN-1998 (TREMBLREL. 05, CD40-ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                    PRELIMINARY;
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61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 CKREILA-LQVYC 116
                                                                                                210 CKVLRLGDLMDYC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 CKREILA-LQIYC 117
                                                                                                                         1 CKRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CKRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
                                           Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC-FINGER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                               Query Match
                                                                                                                                                                                   LT 9
013947
013947;
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Q60803
Q60803;
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TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK,
GILL, DOUGHERTY, NELSON, QUACKENBUSH, 2HOU, KIRKNESS, PETERSON, LOFTUS,
RICHARDSON, DODSON, KHALAK, GLODEK, MCKENNEY, FITZEGERALD, LEE, ADAMS,
HICKEY, BERG, GOCAYNE, UTTERBACK, PETERSON, KELLEY, COTTON, WEIDMAN,
FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY, KARP, SMITH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK, GILL, DOUGHERTY, NELSON, QUACKENBUSH, ZHOU, KIRKNESS, PETERSON, LOFTUS, RICHARDSON, DODSON, KHALAK, GLODEK, WEKENNEY, FTIZEGERALD, LEE, ADAMS, HICKEY, BERG, GOCAYNE, WIELERACK, PETERSON, KELLEY, COTTON, WEIDMAN, FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY, KARP, SMITH, SUBMITTED (AUG.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL, AE000533; G2313200; -.
                                                                                                                                                                                                                                                PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                 AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,
ITOH T., KASAI H., KASHIMOTO K., KIMURA S., KITAKAWA M.,
KITAGAWA M., MAKINO K., MIKI T., MISOBUCHI K., MORI H., MORI T.,
MOTOMURA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S.,
TAGAMI H., TAKEDA J., TAKEMOTO K., TAKEUCHI Y., WADA C.,
YAMAMOTO Y., HORIUCHI T.,
DNA RES. 3.363-377(1996).
EMBL; D90791; G1742452; -.
SEQUENCE 70 AA; 8418 MW; 258BF342 CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O24934 PRELIMINARY; PRT; 231 AA. O24934; 01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) WPOTHETICAL 27.1 KD PROTEIN.
                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 9; LA
Pred. No. 1.96e+00;
2; Mismatches 4
                                                                                                              70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
                                                                                                                                                 CREATED)
                                                                                                                PRT;
                                                                                                                                                02,
03,
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRASER VENTER.;
NATURE 388:539-547(1997).
                                                                                                                                            01-FEB-1997 (TREMBLREL. 01-FEB-1997 (TREMBLREL. 01-MAY-1997 (TREMBLREL. SIMILAR TO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||||
2 KRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 RRAMLMTARNYC 28
            123 CRRTVLSGLD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                             1 CKRAMLAGLN 10
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                 ESCHERICHIA COLI.
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                                                                                                           P76875
P76875;
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PCT-US98-16719-16.rspt

EUTHERIA; PRIMATES

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                                                                                                                                                         TRAF3 OR TRAFAMN.
MUS MUSCULUS (MOUSE),
EUKRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ROEBYIEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 10; Length 567;
Pred. No. 1.96e+00;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 567;
                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J; TISSUE-BRAIN;
WANG X., BORNSLAEGER E., HAUB O., TOMIHARA-NEWBERGER C.,
LONBERG N., DINULOS M.B., DISTECHE C.M., COPELAND N.,
GILBERT D.J., JENKINS N.A., LACY E.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
BMBL, 3033840, G1488198. -
MGD; MGI:108041; TRAF3.
SEQUENCE 567 AA; 64376 MW; 7F4F873B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 13
    PRELIMINARY; PRT; 568 AA.
013114
013114
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AAV-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
CD40 RECEPTOR ASSOCIATED FACTOR 1.
                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 95073988.
HU H.M., O'ROURKE K., BOGUSKI M.S., DIXIT V.M.;
J. BIOL. CHEM. 269:30069-30072(1994).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; U15637; G595911; -.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 2; Le
Pred. No. 1.96e+00;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 AA; 64277 MW; 441E3FC6 CRC32;
            062380 PRELIMINARY; PRT; 567 AA. 062380; OGD-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UF 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION THE RECEPTOR-ASSOCIATED FACTOR 3 (TRAFAMN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
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01,
05,
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ilarity 61.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%;
Similarity 61.5%;
8; Conservative
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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1 CKRAMLAGLNDYC 13
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q12990
Q12990;
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                              CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.; SCIBNCE 267:1494-1498(1995).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL, U21092; G726088; -.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQOINE HERPESVIRUS TYPE 2 (EHV-2).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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MEDINE; 95302501.
TELEPORD E.A., WATSON M.S., AIRD H.C., PERRY J., DAVISON A.J.;
J. MOL. BIOL. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 568;
                                                                                                                                                                                                             Indels
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TELFORD E.A.R.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIEFF E.;
CELL 80:389-399(1995).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
BEBL; U19260; G675460; -.
PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                       Score 57; DB 2; Len
Pred. No. 1.96e+00;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 AA; 64490 MW; 073D0015 CRC32;
                                                                                                                                        568 AA; 64460 MW; 77A8CBDB CRC32;
                                                                                                                                                                                                                                                                                                                                                      568 AA.
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Q66621
Q66621
Q66621
01-NOV-1996 (TREMBLREL. 01, CR
01-NOV-1996 (TREMBLREL. 01, LA
01-NOV-1996 (TREMBLREL. 01, LA
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Similarity 61.5%;
8; Conservative
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Similarity 61.5%;
8; Conservative
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01-NOV-1996 (TREMBLREL. 0)
01-NOV-1998 (TREMBLREL. 05
LMP1 ASSOCIATED PROPIEN. OF
HOMO SAPIENS (HUMAN).
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TISSUE-LYMPHOID TUMOR;
MEDLINE; 95163092.
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1 CKRAMLAGLNDYC 13
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Best Local Similarity
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Best Local Similarity
SEQUENCE FROM N.A. MEDLINE; 95184010.
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                                                                                                                      ZINC-FINGER
SEQUENCE
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DR EMBL; U20824; G695190; -.
SQ SEQUENCE 257 AA; 29138 MW; 3EF159DE CRC32;
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; 0 Query Match 52.3%; Score 56; DB 11; Length 257; Best Local Similarity 54.5%; Pred. No. 3.15e+00; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps

Db 114 NRALLEGLTNY 124 :||:||:| Oy 2 KRAMLAGLNDY 12

Search completed: Fri Sep 25 13:15:10 1998 Job time : 15 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Sep 25 13:12:32 1998; MasPar time 6.05 Seconds 16.575 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-14 (1-4) from PCTUS9816719A.pep 32 1 MLDG 4 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 18.687; Variance 14.983; scale 1.247 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02
	Description	30S RIBOSOMAL PROTEIN	HYPOTHETICAL 11.1 KD P	HYPOTHETICAL 16.6 KD P	TAIL TUBULAR PROTEIN A	HYPOTHETICAL PROTEIN I	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL PROTEIN H	HYPOTHETICAL 27.0 KD P	HYPOTHETICAL 27.1 KD P	HYPOTHETICAL 27.1 KD P	HYPOTHETICAL ABC TRANS	HYPOTHETICAL 32.6 KD P	HYPOTHETICAL TRANSCRIP	ALCOHOL DEHYDROGENASE	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN H	HYPOTHETICAL 46.7 KD P	DIHYDROOROTASE (EC 3.5	HYPOTHETICAL PROTEIN M	C-14 STEROL REDUCTASE	ATP-DEPENDENT DNA HELI	PEPTIDE CHAIN RELEASE
	ឧ	RS7_STAN	Y4EI_RHISN	YYBD_BACSU	VTTA_BPT7	YNHA_RHOER	YHJB_ECOLI	YG21_HAEIN	YFIP_ECOLI	YAT9_SCHPO	YHJQ_ECOLI	Y304_MYCPN	YOSG_MYCTU	YNEJ_ECOLI	ADHI_RHOSH	Y039_MYCGE	Y039_MYCPN	YCIM_HAEIN	YEBA_ECOLI	PYRC_LACLE	YO47_METJA	ERG3_NEUCR	RECQ_BACSU	RF3_ECOLI
	98	-	П	н	٦	٦	ч	Н	-	Н	-	Н	ч	Н	Н	-	Н	п	ч	Н		-1		-
	Length	42	103	147	196	199	200	206	240	240	242	270	289	293	376	384	384	396	419	427	435	490	496	528
æ	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	35	32	32	32
	Result No.	7	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02	1.22e+02
PEPTIDE CHAIN RELEASE		HYPOTHETICAL 67.8 KD P	PUTATIVE MULTICOPPER O	TETRACYCLINE RESISTANC	MINOR VIRION STRUCTURA	MINOR VIRION STRUCTURA	HYPOTHETICAL 88.1 KD P	AMINE OXIDASE PRECURSO	HYPOTHETICAL 83.4 KD P	COPPER AMINE OXIDASE P	PROBABLE DNA-DIRECTED	PROBABLE DNA-DIRECTED	VP3 CORE PROTEIN.	VP3 CORE PROTEIN.	PUTATIVE DNA POLYMERAS	SSM4 PROTEIN.	PROBABLE CALCIUM-TRANS	DNA TOPOISOMERASE II,	RNA POLYMERASE (EC 2.7	TALIN.
RF3_SALTY	ASN1_PEA	YCBB_ECOLI	YAK8_SCHPO	TETQ_BACFR	VM1_REOVL	VM1_REOVD	YNZ8_YEAST	AMO_KLEAE	YOT2_CAEEL	AMO_ECOLI	RPOB_NPVAC	RPOB_NPVOP	VP3_EHDVA	VP3_EHDV1	DP3A_MYCTU	SSM4_YEAST	ATC5_YEAST	TOPB_HUMAN	RRPO_TACV	TALL_MOUSE
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528	585	615	622	641	736	736	754	755	757	757	876	884	899	899	1184	1319	1571	1626	2210	2541
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32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
24	5 6	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

; 42 AA.	TED) SEQUENCE UPDATE) ANNOTATION UPDATE) FRAGMENT).	COCCI; MICROCOCCACEAE.	ENCE FROM N.A. IN-NCTC 8325; A., WATANABE H.; ITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. ITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF SIMILARITY: BELOSOMAL RNA (BY SIMILARITY). SIMILARITY: BELOSOMAL S7 PAMILY OF RIBOSOMAL PROTEINS. 1 UZ0869; G706922; TITE: PSO0052; RIBOSOMAL S7; PARTIAL. SOMAL PROTEIN: RNA-BINDING. 42 42 ENCE 42 A3; 4723 MW; D0130A32 CRC32;	32; DB 1; Length 42; No. 1.22e+02; Mismatches 0; Indels 0; Gaps	; 103 AA.	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) ROTEIN 14EI.	34). SCOTOBACTERIA; AEROBIC RODS AND COCCI;
PRT;	CREATED) LAST SEQUENCE LAST ANNOTATI S7 (FRAGMENT)	OCCI; MI	1.7 TO EMBL/GENBANK/ IN S7 BINDS SPECIF NA (BY SIMILARITY) 20,6 TO THE S7P FA 12,5 TIBOSOMAL_S7; PARTI RNA-BINDING. 472 4723 MW; D0130A32	Score; Pred.	PRT;	CREATED) LAST SEQUENC LAST ANNOTAT PROTEIN Y4EI.	N
STANDAR	(REL. 33, CRE (REL. 33, LAS (REL. 33, LAS AL PROTEIN S7	·	SEQUENCE FROM N.A. STRAIN-NCTC 8325; WADA A., WATANBE H.; STRAINTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA STRAINTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA STRAINTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA STRAINTARITY: BELONGS TO THE S7P FAMILY OF RISEABL, U20869; G706522; PROSITE; PSO0052; RIBOSOMAL_S7; PARTIAL. PROSITE; PSO0052; RIBOSOMAL_S7; PARTIAL. RIBOSOMAL PROTEIN; RRNA-BINDING. NOW_TERR 42 AA; 4723 MW; D0130A32 CRC32;	100.0%; milarity 100.0%; Conservative 34	STANDAR	(REL. 35, (REL. 35, (REL. 35, L 11.1 KD P	z · 5
RESULT 1 ID RS7_STAAU AC P48940;	01-FEB-1996 (REL. 33, 01-FEB-1996 (REL. 33, 01-FEB-1996 (REL. 33, 33, 30S RIBOSOMAL PROTEIN	RPSG. STAPHYLOCOCCUS AUREUS	[1] SEQUENCE FROM N.A. STRAIN-NCTC 8325, WADA A., WATANABE SUBMITTED (FEB-199 -1- FUNCTION: PROT -1- SIMILARITY: BE EMBL, U20869; G706 PROSCITE: PSOHO52; RIBOSOMAL PROTEIN; NOW TER SEQUENCE 42 AA;	Ouery Match Best Local Similarity Matches 4; Conser 31 MLDG 34	RESULT 2 ID Y4EI_RHISN AC P55432;	01-NOV-1997 01-NOV-1997 01-NOV-1997 HYPOTHETICAL	THIZOBLUM SP. (STRAI PLASMID SYM PNGR234A PROKARYOTA; GRACILIC RHIZOBIACEAE. [1] SEQUENCE FROM N.A.
RES ID AC	001	8 8 8 8	RAR B C C C C E E E E E E E E E E E E E E E	ON AG	RES ID	58888	2000 S 8 8

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183 MLDG 186
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                             1 MLDG 4
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P20771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                      Gaps
MEDLINE; 97305956.
REPIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A., PERRET X.;
NATURE 387:394-401(1997).
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                                                                                                                                                                                                                   01-OCT-1994 (REL. 30, CREATED)
1-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDVATION UPDATE)
HYPOTHETICAL 16.6 KD PROTEIN IN COTF-TETB INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 147; Pred. No. 1.22e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 1; Length 196;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                               Score 32; DB 1; Length 103;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          STRAIN=168;
MEDLINE: 96051385.
0GASGWARA N., NAKAI S., YOSHIKAWA H.;
DINA RES. 1:1-14(1944).
-!- SIMILARITY: BELONGS TO THE UPF0039 FAMILY (ELAA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIOPHAGE T7.
VIRIDAE: DS-DNA NONENVELOPED VIRUSES; PODOVIRIDAE.
                                     -i- SIMILARITY: NONE OBVIOUS.
EMBL, AE000071; G2182377; -.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE; PLASMID.
13 57 POTENTIAL.
SEQUENCE 103 AA; 11116 MW; BIFABDES CRC32;
                                                                                                                                                                                                                                                                                                                                                         EMBL; D26185; G467353; -.
SUBTILIST; BG10027; YYBD.
HYPOTHETICAL PROTEIN.
SEQUENCE 147 AA; 16564 MW; 290BCD8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA; 22289 MW; 5F0EB013 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
TAIL TUBULAR PROTEIN A.
                                                                                                                                                                                                  147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 83241725.
DUNN J.J., STUDIER F.W.;
J. MOL. BIOL. 166:477-535(1983).
EMBL; V01146; G15605;
PIR; A04371; TLBPA7.
PIR; $42327; $42327.
                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 MLDG 133
                                                                                                                                       30 MLDG 33
                                                                                                                                                                               3
YYBD_BACSU
P37500;
01-0-1
                                                                                                                                                   1 MLDG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLDG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 4
VTTA_BPT7
P03746;
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YHJB_ECOLI STANDARD; PRT; 200 AA.
P37640;
01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST NNOVATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TREP-KDGK INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFIA H.J., BURLAND V., DANIELS D.L., PLUNKETT G. III, BLATTNER F.R.; NUCLEIC ACIDS RES. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                 01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN IN NITRILE HYDRATASE SUBUNIT ALPHA 5'REGION
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EMBL; U00039; G46657; -.

EMBL; AD000428; G178937; -.

ECOGENE; E512246; W198.

PROSITE; PS00622; HTH_LUXR_FAMILY; 1.

PROSITE: PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.

HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.

"" 159 178 H-T-H MOTIF (BY SIMILARITY).

"" 178 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 32; DB 1; Length 200; Best Local Similarity 100.0%; Pred. No. 1.22e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 199;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                           RHODOCOCCUS ERYTHROPOLIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM
                                                                                                                                                                                                                                                                                                                                                             IKEHATA O., NISHIYAMA M., HORINOUCHI S., BEPPU T.; EUR. J. BIOCHEM. 181:563-570(1989).
EUR. X14668, G809752; -.
EMBL; X1464711; S04471.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1 SEQUENCE 199 AA; 21123 MW; F96CF67A CRC32;
199 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
STANDARD;
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 94316500.
                                                                                                                                                                                                                                                                                                        STRAIN-N-774;
MEDLINE; 89276338.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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143 MLDG 146
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                                                                                                         1 MLDG 4
                                                                                                                                                                               LT 9
YAT9_SCHPO
Q10154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLDG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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SEQUENCE FROM N.A.
STAIN-KIZ / MG1655;
STAIN-KIZ / MG1655;
BLATINER F.R., PLUNKEIT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITIED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; D6404; G987652; -.
EMBL; D6404; G1788937; -.
                                                                                                                                                        HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                   STRAIN-ED / KW201.

MEDLINE: 95350630.

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FLEISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIENCE 269:496-512(1995).
-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL: U32832; 15574470; -.
TIGR: H11621; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YFIP_ECOLI STANDARD; PRT; 240 AA.
047319;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.0 KD PROTEIN IN UNG-PSSA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 206;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12;
NASHIMOTO H., SAITO N.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BC2BA8DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA; 27004 MW; 4D47A994 CRC32;
                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN HI1621.
                      206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
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                      PRT;
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ECOGENE: AE000344; G1788937; --
ECOGENE: EG14233; FFIP.
HYPOTHETICAL PROTEIN.
SEQUENCE 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
larity 100.0%;
Conservative
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                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN;
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72
94 1
136 1
165 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                               PROKARYOTA; GRAC
PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 MLDG 158
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                  YG21_HAEIN
P44274;
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TRANSMEM
TRANSMEM
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TRANSMEM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 94316500.
SOFIA H.J., BURLAND V., DANIELS D.L., PLUNKETT G. III, BLATINER F.R.;
NUCLEIC ACIDS RES. 22:2576-2586(1994).
EMBL; U00039; G466673; -..
EMBL; AE000430; G1789955; -.
ECOGENE; EG12261; YHJQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHJO_ECOLI STANDARD; PRT; 242 AA.
P37555;
01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.1 KD PROTEIN IN DCTA-DPPF INTERGENIC REGION (F242B)
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-972;
STRAIN-972;
STRAIN-972;
STRAIN-972;
STRAIN-972;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z69239; E220668; --
HYPOTHETICAL PROTEIN.
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Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1; Length 242;
Pred. No. 1.22e+02;
Score 32; DB 1; Length 240;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                 i.
                                                                                                                                                                                                                                          01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.1 KD PROTEIN CID4.09C IN CHROMOSOME
SPACID4.09C.
                                                                                                                                                                                                                                                                                                                                                     SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA; 27140 MW; 6CB544E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0EDDC162 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 AA.
                                                                                                                                                                                                          240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                          PRT;
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Y304_MXCPN STANDARD;
Y3535;
O1-NOV-1997 (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA; 27057 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
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Best Local Similarity 100.0%;
Matches 4; Conservative
Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN SEQUENCE 242 AA;
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ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
ID Y3
AC P7
DT 01
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PCT-US98-16719-14.rsp

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A LEMOTO K., INDA T., FUJITA K., HAVASHI K., HONJO A., HORIUCHI T.,
A LIBA H., BABA T., INDA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
REMOTO K., INDA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
RASHIMOTO K., MIKI S., KIMURA S., KITAGAMA M., KITAKAWA M., MAKANO K.,
AN ANSULA S., MIKI T., MAZOBUCHI K., MORI H., MOTOMURA K.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
A TAGAMI H., TAKEMOTO K., WADA C., YAMONO Y., YANO M.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

I. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.

EMBL; D90796; G1742509; -.
REML; D80796; G1742509; -.
REML; D90796; G174250
     STRAIN=K12 / MG1655;
BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BARBER R.D., ROTT M.A., DONOHUE T.J.;
J. BACTERIOL. 178:1386-1393(1996).
-!- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NADH.
-!- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) =
S-FORMIGLIOTATHIONE + NADH.
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
4LCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1) (SLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1) (FDH) (GSH-FDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
W, ADBC8B97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHODOBACTER SPHAEROIDES (RHODOPSEUDOMONAS SPHAEROIDES).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 293
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.22e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 21
62 21
92 21
95 21
98 21
106 21
170 39974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL. 35, CREATED)
(REL. 35, LAST SEQU
(REL. 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2.4.1;
MEDLINE; 96200109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHODOSPIRILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 MLDG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLDG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADHI_RHOSH
P72324;
                                                                                                                            STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULIATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXAB-MARR INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: SOME, TO ALCALIGENES EUTROPHUS 2,4-DICHLOROPHENOXYACETATE MONOOXYGENASE (TFDA).
EMBL: 274410; E249409; -.
HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.
SEQUENCE 289 AA; 32641 MW; 041CB10E CRC32;
                                                                                                                                                                                                                                                                                     HENCHEL ACIDS:

NUCLEIC ACIDS:

NUCLEIC ACIDS:

SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).

EMBL: AE000040; G1674092; -...

PROSITE; PS00211; ABC_TRANSPORTER; 1.

PROSITE; PS00211; ABC_TRANSPORTER; 1.

PROSITE; PS07211; ABC_TRANSPORTER; 1.

RYPOTHEFICAL PROFEIN; ATP-BINDING; TRANSPORT.

NP_BIND

36

43

ATP (POTENTIAL).

SEQUENCE 270 AA; 30770 MW; DF4717F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                   PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES;
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG304 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE: 97105885.
HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 270;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 1; Length 289;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (REL. 34, CREATED)
01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 32.6 KD PROTEIN CY251.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative
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Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                       MYCOPLASMA PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                          MYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 MLDG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 MLDG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37RV;
                                                                                                                                                                                                                                                                             HERRMANN R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLDG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLDG 4
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P77309;
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Gaps

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Length 293;

8

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DDT REAR READER
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Gaps

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Length 376; 0; Indels

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TO SECURCE FROM N.A.

STRAIN—ATCC 33530 / G-37;

SX MEDLINE; 96026346.

RA FRASER C.M., GOCKTNB J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

RA FRASER C.M., GOCKTNB J.D., WHITE O., ADAMS M.D., CLAYTON G., KELLEY J.M.,

RA FLEISCHMANN T.E., BULT C.J., KERLAVGE A.R., SUTTON G., KELLEY J.M.,

RA FRITCHMAN J.L., WEIDMAN J.F., SANDEK D.M., PHILLIPS C.A., MERRICK J.M.,

RA TOWNEN D.T., UTTERBACK T.R., SANDEK D.M., PHILLIPS C.A., MERRICK J.M.,

RA TOWN J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,

RA PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;

SCIENCE 270:397-403(1995).

RR SCIENCE 270:397-403(1995).

RR STICK; MG039; --.

SR HYPOTHETICAL PROTEIN.

SCOUGNICE 384 AA; 42795 MW; BEF2CA8F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOPLASMA GENITALIUM.
PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES;
MYCOPLASMATACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 1; Length 384;
Pred. No. 1.22e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   Y039_MYCGE STANDARD; PRT; 384 AA. 44728.7 (19728.7 (1972.1996 (REL. 34, CREATED) (1972.1996 (REL. 34, LAST SEQUENCE UPDATE) (1972.1996 (REL. 34, LAST SEQUENCE UPDATE) (1972) (1972) (1973) (1973) (1973) (1973) (1973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
127 MLDG 130
|||||
| MLDG 4
                                                                                                                                                                                                                                                   RESULT

YOU

ACCOUNT

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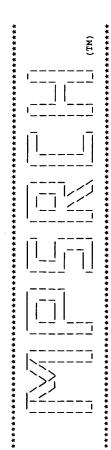
Search completed: Fri Sep 25 13:12:41 1998 Job time : 9 secs.

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0; Gaps

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Sep 25 13:14:29 1998; MasPar time 2.86 Seconds 113.842 Million cell updates/sec Run on:

>PCT-US98-16719-16 (1-13) from PCTUS9816719A.pep 107

Tabular output not generated.

Description: Perfect Score: Sequence:

1 CKRAMLAGLNDYC 13

PAM 150 Gap 15

Scoring table:

69111 segs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 27.495; Variance 30.842; scale 0.891 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description Descripti			ď					
65 60.7 73 1 DISG_TRIGA DISINTEGRIN TRIGRAMIN 165 60.7 73 1 DISB_TRIGA DISINTEGRIN TRIGRAMIN 162 57.9 32 1 V25_HPVLA REGULATORY PROTEIN E2. 58 54.2 356 1 V356_ASFB7 L356 PROTEIN RCHISTAIN 25 51.4 308 1 BEL1_SFV1 ROTEIN. C. 55 51.4 308 1 BEL1_SFV1 ROTEIN ROTEIN RCHISTAIN 25 51.4 354 1 YZ04_METJA HYPOTHETICAL PROTEIN M 25 51.4 552 1 NADE_RHOCA HYPOTHETICAL PROTEIN M 25 51.4 580 1 CG13 YEAR GROWTH FACT 25 51.4 580 1 CG13 YEAR GROWTH FACT 25 51.4 50.5 271 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 50.5 271 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 50.5 304 1 SPEB_SCHPO PUTATIVE AGMATITASE PR 4 50.5 304 1 SPEB_SCHPO PUTATIVE AGMATITASE PR 4 50.5 625 1 FANA_HELAS FARFAMIDE—ACTIVATED AM 4 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR2_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 6 50.5 906 1 GLR1_HUMAN GLUTAMATE	Result No.	Score	Ouery Match	Length	DB	ព្	Description	Pred. No.
65 60.7 73 1 DISB_TRIGA DISINTEGRIN TRIGRAMIN 1 62 57.8 49 1 DISI_CENCA DISINTEGRIN TRIGRAMIN 1 62 57.9 32 1 V25_ASFB7 BEGULATORY PROTEIN E2. 58 51.4 308 1 BEL_1SFV1 BEL-1 PROTEIN E2. 55 51.4 308 1 BEL_1SFV1 SYD FROTEIN E2. 55 51.4 308 1 YZO4_METJA HYPOTHETICAL PROTEIN E2. 55 51.4 439 1 YZO4_METJA HYPOTHETICAL PROTEIN M 2. 55 51.4 550 1 K204_METJA HYPOTHETICAL PROTEIN M 2. 55 51.4 580 1 K204_METJA HYPOTHETICAL PROTEIN M 2. 55 51.4 580 1 K204_METJA HYPOTHETICAL PROTEIN M 2. 55 51.4 580 1 K204_METJA HYBOTHETICAL PROTEIN M 2. 55 51.4 50.5 1 RNK_HUMAN RIBONCLEASE KG PREUR 4. 50.5 271 1 RBPS_MOUSE INSULIN-LIKE GROWTH FA. 50.5 394 1 SPEB_SCHPO PUTATIVE AGMATITASE PR 4. 50.5 304 1 SPEB_SCHPO PUTATIVE AGMATITASE PR 4. 50.5 625 1 FANA_HELAS FWERMIDE-ACTIVATED AM 4. 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4. 50.5 902 1 GLR2_HUMAN GLUTAMATE RECEPTOR 4 P 4. 50.5 906 1 GLR2_HUMAN GLUTAMATE RECEPTOR 1 P 4. 50.5 906 1 GLR2_HUMAN GLUTAMATE RECEPTOR 1 P 4. 50.5 906 1 GLR2_HUMAN GLUTAMATE	н	65	60.7	73	: -	DISG_TRIGA		1.69e-02
64 59.8 49 1 DISI_ECHCA DISINTEGRIN ECHISTATIN 2 5 57.9 322 1 VE2_HPV1A REGULATORY PROTEIN E2. 8 54.2 356 1 VE2_HPV1A REGULATORY PROTEIN E2. 8 54.2 308 1 BELI_SFV1 BEL-1 PROTEIN. 2 5 51.4 354 1 YZCU_YERPS YOP PROTEIN. 2 5 51.4 439 1 YZCU_YERPS YOP PROTEIN. 2 5 51.4 520 1 NADE_RHOCA NH(3)-DEPENDENT NADL(+) S 5 51.4 812 1 FGR1_XENLA HYPOTHETICAL PROTEIN N 2 5 51.4 812 1 FGR1_XENLA HYPOTHETICAL PROTEIN N 2 5 51.4 812 1 FGR1_XENLA HYPOTHETICAL PROTEIN N 2 5 51.4 812 1 FGR1_XENLA HYPOTHETICAL CYCLIN C 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	7	65	60.7	73	Н	DISB_TRIGA		1.69e-02
62 57.9 322 1 VEZ_HPV1A REGULATORY PROTEIN E2. 8 55 51.4 356 1 VEZ_HPV1A REGULATORY PROTEIN E2. 8 55 51.4 354 1 YSCU_YERPS COPPLEY. 55 51.4 354 1 YSCU_YERPS COP PROTEIN. 55 51.4 4 39 1 YZOU_YERPS COP PROTEIN TRANSLOCA 2 55 51.4 552 1 WADE_RHOCA N(3)-DEPENDENT NAD(+) Z 55 51.4 580 1 CG13_YERJA HYPOTHETICAL PROTEIN M 2 55 51.4 580 1 CG13_YERJA GI/S-SPECIFIC CYCLIN C 54 50.5 51.4 812 1 FGR1_XENLA FIBROBLAST GROWTH FACT 2 54 50.5 571 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 571 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 51 1 SPEB_RAT INSULIN-LIKE GROWTH FA 4 50.5 51 1 SPEB_ZGHPO UTATIVE AGNATINASE PR 4 50.5 625 1 FANA_HELAS FRREMIDE-ACTIVATED AM 5 54 50.5 883 1 GLRZ_MOUSE GUUTAMATE RECEPTOR 2 P 4 50.5 625 1 GLRZ_HUMAN GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLRZ_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLRZ_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLRZ_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLRZ_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLRZ_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 907 1 GLRZ_HAM GLUTAMATE RECEPTOR 1 P 4 50.5 907 1 GLRZ_HAM GLUTAMATE RECEPTOR 1 P 4 50.5 907 1 GLRZ_HAM GLUTAMATE RECEPTOR 1 P 4 50.5 907 1 GLRZ_HAM GLUTAMATE RECEPTOR 1 P 4 50.5 907 1 GLRZ_HAM GLUTAMATE RECEPTOR 1 P 4	٣	64	59.8	4	٦	DISI_ECHCA	DISINTEGRIN ECHISTATIN	2.89e-02
58 54.2 356 1 V356 ASFB7 L356 PROTEIN. 55 51.4 308 1 BELL_SFV1 BELL_SFV2 RDL-PROTEIN. 55 51.4 439 1 X20L_YERS YOP PROTEIN TRANSLOCA 2 55 51.4 439 1 X20L_METJA HYPOTHETICAL PROTEIN M 2 55 51.4 52 1 NADE_RHOCA HYBOTHETICAL PROTEIN M 2 55 51.4 50 1 CALL_XENLA HYBOTHETICAL PROTEIN M 1 54 50.5 51.4 812 1 FGRI_XENLA FIBROBLAST GROWTH FACT 2 54 50.5 271 1 RNEG_HUMAN RIBONGHTH FACT 2 54 50.5 271 1 IBPS_RAT INSULIN-LIKE GROWTH FA 4 54 50.5 34 1 SPEB_SCHPO PUTATIVE AGMATIRASE PR 4 54 50.5 625 1 FANA_HELAS FARFAMIDE-ACTIVATED AM 5 54 50.5 883 1 GLR2_MUMA GLUTAMATE RECEPTOR 2 P 4	7	62	57.9		ч	VE2_HPV1A		8.31e-02
S5 S1.4 308 1 BELL_SFV1 BEL-1 PROTEIN. S5 S1.4 354 1 YSCU_TERPS YOP PROTEIN. S5 S1.4 4 354 1 YSCU_TERPS YOP PROTEIN TANNSLOCA S5 S1.4 4 552 1 NADE_RHOGA NH(3) -DEPENDENT NAD(+) S5 S1.4 S1.2 1 S2.2 1 YEAST S1.4 S1.5 S1.4 S6 S1.4 S1.2 1 YEAST S1.4 S1.5 S1.4 S6 S1.4 S1.2 1 YEAST S1.4 S1.5 S1.4 S6 S1.4 S1.2 1 IBP5_MOUSE INSULIN-LIKE GROWTH FRA S6 S0.5 S1.1 IBP5_RAT INSULIN-LIKE GROWTH FRA S6 S0.5 S1.1 ISP5_RAT GLUTAMATE RECEPTOR 2 P S6 S0.5 S1.1 ISP5_RAT GLUTAMATE RECEPTOR 4 P S6 S0.5 S0.5 GLR4_RAT GLUTAMATE RECEPTOR 4 P S6 S0.5 S0.5 GLR4_RAT GLUTAMATE RECEPTOR 1 P S6 S0.5 S0.5 GLR4_RAT GLUTAMATE RECEPTOR 1 P S6 S0.5 S0.5 GLR4_RAT GLUTAMATE RECEPTOR 1 P S6 S0.5 GLR4_RAT GLRAT GLATAMATE RECEPTOR 1 P S6 S0.5 GLRAT GLATAMATE RECEPTOR 1 P	Ŋ	28	54.2	356	٦	V356_ASFB7	L356 PROTEIN.	6.42e-01
55 51.4 354 1 YSCU_YERPS YOP PROTEINS TRANSLOCA 25 51.4 439 1 YZOU_YERPS YOP PROTEINS TRANSLOCA 25 51.4 439 1 YZOU_YETJA HYPOTHETICAL PROTEIN M 25 21.4 580 1 CG13_YERJS G1/S_SPECIFIC CYCLIN C 25 21.4 812 1 FGRI_XENLA FIBNOBLAST GROWTH FACT 2 2 1 RNG_HUMAN RIBONUCLEASE KG PRECUR 4 50.5 271 1 RPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 394 1 SPEB_SCHPP PUTATIVE AGMATINASE PR 4 50.5 394 1 SPEB_SCHPP PUTATIVE AGMATINASE PR 4 50.5 883 1 GLRZ_MOUSE GLUTAMATE RECEPTOR 2 4 50.5 883 1 GLRZ_HUMAN GLUTAMATE RECEPTOR 2 4 50.5 883 1 GLRZ_HUMAN GLUTAMATE RECEPTOR 2 4 50.5 902 1 GLR4_ART GLUTAMATE RECEPTOR 4 4 50.5 905 1 GLR4_LART GLUTAMATE RECEPTOR 4 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 7 7 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 7 7 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 7 7 7 7 7 7 7 7 7	9	55	51.4	308	П	BEL1_SFV1	BEL-1 PROTEIN.	2.79e+00
55 51.4 439 1 X204 METJA MYPOTHETICAL PROTEIN M 25 51.4 552 1 0.04 METJA MYROTHETICAL PROTEIN M 25 51.4 552 1 0.04 METJA MYROTHETICAL PROTEIN M 25 51.4 500 1 FGR1_XENLA FIBROBLAST GROWTH FACT 25 51.4 51.5 1 RNKE_HUWAN RIBONOTLEASE KG PRECUR 45 50.5 271 1 RPS_MOVE INSULIN'-LIKE GROWTH FA 54 50.5 394 1 SPEB_SCHPO PUTATIVE ACMATITIASE PR 45 50.5 625 1 FANA_HELAS FWRFAMIDE-ACTIVATED AM 54 50.5 633 1 GLR2_MOVE GLUTAMATE RECEPTOR 2 24 50.5 633 1 GLR2_LHUMAN GLUTAMATE RECEPTOR 2 24 50.5 632 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 24 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 24 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 7 7 4 7 6 7 6 7 7 7 7 7 7	7	55	51.4	354	-	YSCU_YERPS	YOP PROTEINS TRANSLOCA	2.79e+00
55 51.4 55.2 NADE_RHOCA NH(3)-DEPENDENT NAD(+) 25.5 51.4 580 CG13_YEAST GL/S-SPECIFIC CYCLINC C 25.5 51.4 51.0 CG13_YEAST GL/S-SPECIFIC CYCLINC C 25.5 51.4 61.0 1 EPGL_HUMAN RIBONUCLEAST GROWTH FACT 2 54.5 50.5 271 1 IBP5_MOUSE INSULIN-LIKE GROWTH FA 4 5 0.5 371 1 IBP5_MATE INSULIN-LIKE GROWTH FA 4 5 0.5 371 1 IBP5_MATE INSULIN-LIKE GROWTH FA 4 5 0.5 371 1 IBP5_MATE INSULIN-LIKE GROWTH FA 4 5 0.5 371 1 IBP5_MATE INSULIN-LIKE GROWTH FA 4 5 0.5 383 1 GLR2_MATE CLUTAMATE RECEPTOR 2 P 4 5 0.5 383 1 GLR2_MATE GLUTAMATE RECEPTOR 2 P 4 5 0.5 392 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 5 0.5 302 1 GLR2_RAT GLUTAMATE RECEPTOR 4 P 4 5 0.5 302 1 GLR2_RAT GLUTAMATE RECEPTOR 4 P 4 5 0.5 306 1 GLR1_MAN GLUTAMATE RECEPTOR 4 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 5 0.5 307 1 GLR1_MAN GLUTAMATE RECEPTOR 1 P 4 4 0.5 307 1 GLR1_MAN 307 30	ω	52	51.4	439	~	YZO4_METJA		2.79e+00
55 51.4 580 1 CG13_YEAST G1/S-SPECIFIC CYCLIN C 2 55 51.4 812 1 FGR1_XENLA FIBROBLEAST GROWTH FACT 2 54 50.5 150 1 RNK6 HUMAN RIBONUCLEAST GROWTH FACT 2 54 50.5 271 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 374 1 SPEB_SCHPO PUTATIVE AGMATINASE PR 4 50.5 374 1 SPEB_SCHPO PUTATIVE AGMATINASE PR 4 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR2_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR2_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR2_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR2_HAM GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 7 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4	σ	52	51.4	552	-	NADE_RHOCA	NH(3)-DEPENDENT NAD(+)	2.79e+00
55 51.4 812 FGRL XENLA FIBROBLAST GROWTH FACT 54 50.5 150 RNK6_LHWAN RIBONCLEASE KG PRECUR 45 50.5 271 1 RBP5_JHOUSE INSULIN-LIKE GROWTH FA 54 50.5 271 1 RBP5_JHOUSE INSULIN-LIKE GROWTH FA 54 50.5 394 1 SPEB_SCHPO PUTATIVE ACMATINASE PR 45 50.5 625 1 FANA_HELAS FMRFANIDE-ACTIVATED AM 54 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 45 50.5 902 GLR2_RAT GLUTAMATE RECEPTOR 2 P 45 50.5 902 GLR4_AAT GLUTAMATE RECEPTOR 2 P 45 50.5 902 GLR4_AAT GLUTAMATE RECEPTOR 4 P 45 50.5 906 GLR4_HWAN GLUTAMATE RECEPTOR 4 P 45 50.5 906 GLR1_HWAN 906	10	55	51.4	580	-	CG13_YEAST	G1/S-SPECIFIC CYCLIN C	2.79e+00
54 50.5 150 1 RNK6_HUMAN RIBONUCLEASE K6 PRECUR 4 50.5 271 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 271 1 IBPS_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 374 1 SPEB_SCHPO PUTATIVE GROWTH FA 4 50.5 625 1 FANA_HELAS FORFAMIDE-ACTIVATED AM 4 54 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 50.5 883 1 GLR2_MUMAN GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 902 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 907 1 GLR1_HUMA	11	55	51.4		-	FGR1_XENLA	FIBROBLAST GROWTH FACT	2.79e+00
54 50.5 271 1 IBP5_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 271 1 IBP5_MOUSE INSULIN-LIKE GROWTH FA 4 50.5 371 1 IBP5_MOLS INSULIN-LIKE GROWTH FA 4 50.5 374 1 SPEB_SCHPO PUTATIVE AGMATIRASE PR 54 50.5 625 1 FANA_HELAS FMRFAMIDE-ACTIVATED AM 4 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 50.5 906 1 GLR1_HUMAN GLUT	17	54	50.5		٦	RNK6_HUMAN	RIBONUCLEASE K6 PRECUR	4.48e+00
54 50.5 271 1 IBP5_RAT INSULIN-LIKE GROWTH FA 4 54 50.5 394 1 SPEB_SCHPO PUTATIVE AGNATINASE PR 4 54 50.5 62 1 FANA, HELAS FMREMAIDE-ACTIVATED AM 4 54 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 54 50.5 883 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 54 50.5 902 1 GLR4_ART GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR4_HWAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR4_HWAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 906 1 GLR1_HWAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 906 1 GLR1_HWAN GLUTAMATE RECEPTOR 1 P 4	13	54	50.5		-	IBP5_MOUSE		4.48e+00
54 50.5 394 1 SPEB_SCHPO PUTATIVE AGMATINASE PR 4 54 50.5 625 1 FANA, HELAS FMRFANIDE-ACTIVATED AM 4 54 50.5 883 1 GLR2, MOUSE GLUTAMATE RECEPTOR 2 P 54 50.5 883 1 GLR2, HUMA GLUTAMATE RECEPTOR 2 P 54 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 907 1 GLR1, HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1, HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1, HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1, HUMAN GLUTAMATE RECEPTOR 1	14	54	50.5		П	IBP5_RAT	INSULIN-LIKE GROWTH FA	4.48e+00
54 50.5 625 1 FANA_HELAS FMRFANIDE-ACTIVATED AM 4 54 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 54 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 54 50.5 883 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 54 50.5 902 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 54 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 908 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 908 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 54 54 54 54 54 54 54 54 54 54 54 5	15	54	50.5		Н	SPEB_SCHPO		4.48e+00
54 50.5 883 1 GLR2_MOUSE GLUTAMATE RECEPTOR 2 P 4 5 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 5 50.5 883 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 5 50.5 902 1 GLR2_RAT GLUTAMATE RECEPTOR 4 P 4 5 5 905 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 5 5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 5 5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 5 905 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	16	54	50.5		-	FANA_HELAS	FMRFAMIDE-ACTIVATED AM	4.48e+00
54 50.5 883 1 GLR2_HUMAN GLUTAMATE RECEPTOR 2 P 4 5 50.5 883 1 GLR2_HAT GLUTAMATE RECEPTOR 2 P 4 5 5 5 5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 5 4 50.5 906 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 5 4 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 4 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 5 6 5 907 1 GLR1_HOWAN GLUTAMATE RECEPTOR 1 P 4 6 6 5 907 1 GLR1_HOWAN GLUTAMATE RECEPTOR 1 P 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	17	24	50.5		-	GLR2_MOUSE		4.48e+00
54 50.5 883 1 GLR2_RAT GLUTAMATE RECEPTOR 2 P 4 54 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 902 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4	18	54	50.5		Н	GLR2_HUMAN		4.48e+00
54 50.5 902 1 GLR4_RAT GLUTAMATE RECEPTOR 4 P 4 54 50.5 902 1 GLR4_HUWAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR1_HUWAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_MOUSE GLUTAMATE RECEPTOR 1 P 4	19	54	50.5		-	GLR2_RAT		4.48e+00
54 50.5 902 1 GLR4_HUMAN GLUTAMATE RECEPTOR 4 P 4 54 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_MOUSE GLUTAMATE RECEPTOR 1 P 4	50	54	50.5		Н	GLR4_RAT		4.48e+00
54 50.5 906 1 GLR1_HUMAN GLUTAMATE RECEPTOR 1 P 4 54 50.5 907 1 GLR1_MOUSE GLUTAMATE RECEPTOR 1 P 4	21	54	50.5		1	GLR4_HUMAN		4.48e+00
.5 907 1 GLR1 MOUSE GLUTAMATE RECEPTOR 1 P 4	22	54	50.5	906	-	GLR1_HUMAN		4.48e+00
	23	54	50.5	907	Н	GLR1 MOUSE		4.48e+00

4.48e+00	4.48e+00	7.15e+00	7.15e+00	7.15e+00	7.15e+00	7.15e+00	7.15e+00	1.13e+01 1.13e+01													
GLUTAMATE RECEPTOR 1 P	DELTA- (L-ALPHA-AMINOAD	PORPHOBILINOGEN DEAMIN	PUTATIVE VENOM METALLO	ELONGATION FACTOR G, M	HYPOTHETICAL 108.2 KD	SNQ2 PROTEIN.	FATTY ACID SYNTHASE (E	INTERLEUKIN-4 PRECURSO	CHLOROPHYLL A-B BINDIN	ESTERASE CM06B1 (EC 3.	HYPOTHETICAL 163.6 KD	HYPOTHETICAL 207.6 KD									
GLR1_RAT	ACVS_CEPAC	HEM3_PEA	DISA_TRIGA	EFG2_YEAST	YGX7_YEAST	SNQ2_YEAST	FAS_CHICK	IL4_PIG	CB21_SILPR	CB2B_LYCES	CB22_MAIZE	CB21_GOSHI	CB24_PETSP	CB25_NICPL	CB21_WHEAT	CB23_PETSP	CB27_TOBAC	CB2B_PINSY	EST2_CAEEL	YM8B_YEAST	YFA7_YEAST
Н	Н	-		~	н	Н	Н	Н	Н	-	H	Н	Н	Н	-	н	н	-	-	-1	Н
907	3712	369	480	819	958	1501	2511	133	205	265	265	265	266	266	266	267	267	274	556	1420	1804
50.5	50.5	49.5	49.5	49.5	49.5	49.5	49.5	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6
54	24	23	23	53	23	23	23	25	25	25	25	25	25	25	25	25	25	25	25	25	25
24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAB. SCI. U.S.A. 87:2471-2475(1990).
-!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS
EXPRESSED ON GLYCOPROFIN IIB-IIIA COMPLEX. ACT BY BINING TO THE
GLYCOPROFIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
  GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT
           AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR AND COLLAGEN.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND COLLAGEN.
-1- THE SEQUENCE SHOWN IS THAT OF TRIGRAMIN BETA-2.
-1- SIMILARITY: BELONG TO THE FAMILY OF GPILB-ILIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR: C35982; C35982.
                                   SIMILARITY: BELONG TO THE FAMILY OF GPIIB-IIIA PROTEIN ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM. E35982; E35982.
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION
                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                        Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 1; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN BETA-1 FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P17494; 1KST.
PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM.
15 PROBABLE.
                                                                                                                                                                                                                  CELL ATTACHMENT SITE
                                                                                                                                                                                                                                                        Score 65; DB 1; L
Pred. No. 1.69e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.69e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61CBAFCF CRC32;
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                               DA64D759 CRC32
                                                                                                                                                                                                                                                                                                                                                                                   73 AA
                                                                                                                                                    PROBABLE. PROBABLE.
                                                                                                                                                                                          PROBABLE
                                                                                                                                                                                                                                                                   Pred. 1
2; M
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                  53
7573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.8%;
                                                                                                                                                                                                                                                        60.7%;
                                                                                                                                                                                                                                                                   53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%;
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                        47 CRRARGDDLDDYC 59
                                                                                                                                                                                                                                                                                                                               1 CKRAMLAGLNDYC 13
                                                                        PIR; A23731; A23731.
PIR; S43021; S43021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P17494; 1KST.
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90207217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                   FRIGA
                                                                                                                                                   DISULFID
                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                              SEQUENCE
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                                                             PIR;
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Gaps

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4; Indels

2; Mismatches

7; Conservative

Matches

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FEBS LETT. 309:316-320(1992).

-!- FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURFACE AND INHIBIT AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR.
MEDILINE; 92104150.
MEDILIC., WIDMER H., BOVERMANN G., BRECKENRIDGE R., METTERNICH R.;
EUR. J. BIOCHEM. 202:315-321(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND COLLAGEN.

-!- THE SEQUENCE SHOWN IS THAT OF ECHISTATIN ALPHA-1.
-!- SIMILARINY: BELLONG TO THE FAMILY OF GPIIB-IIIA PROTEIN
ANTAGONISTS, CALLED DISINTEGRINS, THAT IS FOUND IN SNAKE VENOM.
PIR, 332592; A35592.
PIR; S29198; S29198.
                                                                                                                     01-AUG-1990 (REL. 15, CREATED)
1-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANDVATION UPDATE)
DISINTEGRIN ECHISTATIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COOKE R.M., CARTER B.G., MARTIN D.M.A., MURRAY-RUST P., WEIR M.P.; EUR. J. BIOCHEM. 202:323-328(1991).
                                                                                                                                                                                                                                                                                        MEDLINE; 89066819.
GAN Z.R., GOULD R.J., JACOBS J.W., FRIEDMAN P.A., POLOKOFF M.A.;
J. BIOL. CHEM. 263:19827-19832(1988).
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 90207217.
DENNIS M.S., HENZEL W.J., PITTI R.M., LIPARI M.T., NAPIER M.A.,
DEISHER T.A., BUNTING S., LAZARUS R.A.;
PROC. NATL. ACAD. SGI. U.S.A. 87:2471-2475(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                            ECHIS CARINATUS (SAW-SCALED VIPER).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILLA;
LEPIDOSAURIA; SERPENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92089067.
CHEN Y., PITZENBERGER S.M., GARSKY V.M., LUMMA P.K., SANYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92387379.
CALVETE J.J., WANG Y., MANN K., SCHAEFER W., NIEWIAROSKI
STEWART G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR.
MEDILINE; 9210415.7.
SAUDEK V., ATKINSON R.A., LEPAGE P., PELTON J.T.;
EUR. J. BIOCHEM. 202:329-338(1991).
                                                                                          49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91308124.
SAUDEK V., ATKINSON R.A., PELTON J.T.;
BIOCHEMISTRY 30:7369-7372(1991).
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOCHEMISTRY 30:11625-11636(1991)
                                                                                          STANDARD;
                   1:|| |:|||
1 CKRAMLAGLNDYC 13
47 CRRARGDDLDDYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92104151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR
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                                                                                                                                                                                                                                                                             TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE-VENOM;
                                                                       LT 3
DISI_ECHCA
P17347;
                                                                                                                                                                                   (CARINATIN)
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      SECUENCE
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CKRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 NRAMLISVKNFC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 91276270.
                                                                                                                                                                              COMPLETE GENOME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN PAPILLOMAVIRUS TYPE 1A.
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES
             PROSITE; PS00427; DISINTEGRINS; 1.
BLOOD COAGULATION; PLATELET; CELL ADHESION; VENOM; 3D-STRUCTURE.
MOD_RES

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-1- SUBUNIT: BINDS DNA AS A DIMER.

EMBL; VOILIG: -; NOT_ANNOTATED_CDS.

PIR: A03665; WZWLE.

FRALY PROFILIY: TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; SEQUENCE 322 AA; 36923 MW. DNA-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DANOS O.;
SUBMITTED (JAN-1985) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: E2 IS A TRANSCRIPTIONAL TRANSACTIVATOR CAPABLE OF
ACTIVATING A CONDITIONAL ENHANCER IN THE VIRAL LONG CONTROL
REGION (LCR). E2 BINDS TO THE 5'-ACCGNNNCGGT-3' PALINDROMIC
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                                                                                                                                                                                                                                                                                                                        Score 64; DB 1; Length 49;
Pred. No. 2.89e-02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 1; Length 322;
Pred. No. 8.31e-02;
3; Mismatches 3; Indels
                                                                                                                                                              CELL ATTACHMENT SITE.
MISSING (IN ALPHA-2 FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20, CREATED)
20, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VE2_H91
VE2_H01A STANDARD; PRT; 322 AA.
VE2_H03118;
21-JUL-1986 (REL. 01, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-J0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
REGULATORY PROTEIN E2.
                                                                                                                                                                                                                                                                                       0A851E33 CRC32;
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                                                                                     PROBABLE.
PROBABLE.
                                                                      FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 84182467.
DANOS O., XATINKA M., YANIV M.;
EMBO J. 1:231-236(1982).
                                                                                     111
332
339
266
49
13
13
32
5424 MW;
                                                                                                                                                                                                                                                                                                                      59.8%;
ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.9%;
Similarity 50.0%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKRAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 KRDILQDLDDFC 312
                                                                                                                                                                                                                                                                                                                                                                                               20 CKRARGDDMDDYC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KRAMLAGLNDYC 13
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P23165;
01-NOV-1991 (REL. 2
01-NOV-1995 (REL. 2
01-NOV-1995 (LEL. 2
L356 PROTEIN.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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REVISIONS.
                                                                                 DISULFID
DISULFID
DISULFID
DISULFID
SITE
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SEQUENCE
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TURN
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STRAND
STRAND
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ID V3
AC P2
DT 01
DT 01
DE L3
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SIMIAN FOAMY VIRUS (TYPE 1) (SFV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
SPUMAVIRINAE.
                                          SEQUENCE FROM N.A.
MEDLINE; 90219205.
GONZĀLEZ A., CALVO V., ALMAZĀN F., ALMENDRAL J.M., RAMIREZ J.C.,
DE LA VEGA I., BLASCO R., VINUĒLA Ē.;
J. VIROL. 64:2073-2081(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUPIEC J.-J., KAY A., HAYAT M., RAVIER R., PERIES J., GALIBERT GENE 101:185-194(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 1; Length 356;
Pred. No. 6.42e-01;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 1; Length 308;
Pred. No. 2.79e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION REGULATION; ACTIVATOR.

CONFLICT 89 80 D -> N (IN REF. 2)

CONFLICT 119 119 D -> N (IN REF. 2)

CONFLICT 257 257 S -> G (IN REF. 2)

SEQUENCE 308 AA: 35311 MW; 96D2D7B2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELL_SV1 STANDARD; PRT; 308 AA. BELL_SV1 STANDARD; PRT; 308 AA. 01-DEC-1992 (REL. 24, CREATED) 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) BEL-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.4%;
Best Local Similarity 53.8%;
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Best Local Similarity 41.7%;
Matches 5; Conservative
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SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDILNE; 95249563.
BUSSEX H., KABACK D.B., ZHONG W., VO D.T., CLARK M.W., FORTIN N.,
HALL J., OUELLETTE B.F.F., KENG T., BARTON A.B., SU Y., DAVIES C.K.,
STORMS R.K.;
                                                                                                                                                                                                                                                                                                                                              MEDLINE: 94253014.
MEDLINE: 94253014.
WILLISON JC., TISSOT G.;
J. BACTERIOL. 176:3400-3402(1994).
-!- FUNCTION: IT NOT KNOWN IF THIS NAD SYNTHASE USES NH(3) OR
GLOTAMINE AS THE N DONOR.
-!- CAPALYTIC ACTIVITY: ATP + DEAMIDO-NAD(+) + NH(3) + H(2)O - AMP + PATHWAY: DE NOVO BIOSYNTHESIS OF NAD.
-!- PATHWAY: DE NOVO BIOSYNTHESIS OF NAD.
-!- SIMILARITY: TO OTHER SPECIES NADE.
EMBL; X59399; G45986; -.
PIRE, SISSES; SISSES:
                                                                                                                                                                NADE OR ADGA.
RHODODSACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 1; Length 552; Pred. No. 2.79e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S673A;
MEDLINE; 89210821.
NASH R., TOKIWA G., ANAND S., ERICKSON C., FUTCHER A.B.;
EMBO J. 7:4335-4346(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (REL. 13, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
61/S-SPECIFIC CYCLIN CLN3.
CLN3 OR WHI1 OR DAFI OR YALO40C OR FUNIO.
SACCHAROMYCES CEREVISIAE (BARRER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 AA; 59706 MW; 58E72EC7 CRC32;
                                                                   552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA
                                                                                                                                                                                                                                                                                                      WILLISON J.C.;
FEMS MICROBIOL. REV. 10:1-38(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CROSS F.R.;
MOL. CELL. BIOL. 8:4675-4684(1988).
                                                RESULT 9
ID NADE_RHOCA STANDARD;
AC 003638;
DT 01-JUN-1994 (REL. 29, LAST SEQUED)
DT 01-OCT-1996 (REL. 34, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 51.4%;
Local Similarity 70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 RAMVLGLQDY 278
                                                                                                                                                                                                                                                                                MEDLINE; 93159814.
WILLISON J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||: || ||
3 RAMLAGLNDY 12
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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   2 KRAMLAGLNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG13_YEAST
P13365;
                                                                                                                                                                                                                                                                     STRAIN-B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                              PROKARYOTA; GRACILLICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLEAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,
SUVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDODOVSKY M.,
SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 1; Length 354;
Pred. No. 2.79e+00;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 1; Length 439;
Pred. No. 2.79e+00;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: SOME, TO M.JANNASCHII MJ0425.
EMBL; L77118; G1500652; -.
TIGR; MJECLO4; -.
TIGR: MJECLO4; -.
NPCOTHETICAL PROTEIN; ATP-BINDING.
NP_BIND 28 35 ATP (POTENTIAL).
SEQUENCE 439 AA; 52421 MW; 7FA7C52D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC150C3F CRC32;
                               01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
YOP PROTEINS TRANSLOCATION PROTEIN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 AA
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PRT;
                                                                                                                                                                                                                                                                                                                              EMBL; L25667; G475126; -- PLASMID; VIRULENCE; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   40381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN MJECL04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                 TERSINIA PSEUDOTUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.4%;
Best Local Similarity 77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                  50
99
158
183
207 ·
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 RKSKLVGLDDY 411
                                                                                                                                                                                                                                                                                                                                                                                                               163
187
254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 96337999.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 AMLMGLSDY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID PIB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YZ04_METJA
Q60260;
YSCU_YERPS
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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FRANSMEM TRANSMEM SEQUENCE

C F F S

Matches

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TRANSMEM

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Gaps

Gaps

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Score 55; DB 1; Length 812; Pred. No. 2.79e+00; 4; Mismatches 0; Indels

POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
; GAFAEGSD CRC32;

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                                                                                                                              Ouery Match 51.4%;
Best Local Similarity 55.6%;
Matches 5; Conservative
         223
236
260
292
313
326
90502
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1 CKRAMLAGLNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 CNRAM-SGINNY 56
        223
236
260
292
313
326
812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
38
61
145
46
60
78
85
150 AA;
                                                                                                                                                                                         449 PMLSGLSEY 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                           :|{:||::|
4 AMLAGINDY 12
      CARBOHYD
CARBOHYD
CARBOHYD
                                                 CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGFR-1.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUSCI T.J., AWAYA E., KIRSCHNER M.W.;

PROC. NATL. ACAD. SCI. U.S.A. 87:8365-8369(1990).

PROC. NATL. ACAD. SCI. U.S.A. 87:8365-8369(1990).

-!- FUNCTION RECEPTOR FOR BASIC FIBROBLAST GROWTH
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR.

-!- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR EXTRACELLULAR DOMAINS CONTAINS 3 IG-LIKE DOMAINS.

-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE EXTRACELLULAR DOMAINS CONTAINS 3 IG-LIKE DOMAINS.

REMBL; M61687; G214138; --

RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                     Gaps
PROC. NATL. ACAD. SCI. U.S.A. 92:3809-3813(1995).

-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G (STATT) TRANSTION. CLIM3 MAY BE AN UPSTREAM ACTIVATOR OF THE G CYCLINS WHICH DIRECTLY CATALYZE START.

-1- INDUCTION: IT IS NOT SIGNIFICANTLY CELL CYCLE REGULATED.

-1- SIMILARITY: TO OTHER CYCLINS. STRONGEST TO OTHER G1/S CYCLINS. EMBL; M23359; G295609; -.

EMBL; M23359; G295599; ALT_TERM.

EMBL; M2359; G295599; ALT_TERM.

EMBL; M2359; G295544; -.

PIR: 514054; S14054.
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                   Score 55; DB 1; Length 580;
Pred. No. 2.79e+00;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
FGF RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTODIASMIC (POTENTIAL).
PROTEIN KIRASE.
IG-LIKE DOMAIN.
IG-LIKE DOMAIN.
IG-LIKE DOMAIN.
ATP (BY SIMILARITY).
ATP (SY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                   PROSITE: PS00292; CYCLINS; 1.
CYCLIN; CELL CYCLE; CELL DIVISION.
SEQUENCE 580 AA; 64990 MW; C84C8B61 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                         812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                   / Match 51.4%;
Local Similarity 36.4%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                              370 KSLLDALQNYC 380
                                                                                                                                                                                                                                                                                                                                 3 RAMLAGLNDYC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 91045998.
                                                                                                                                                                                                                                                                                                                                                                                        LT 11
FGR1_XENLA
P22182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
ACT_SITE
ACT_SITE
ACT_CARBOHYD
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CARBOHYD
CARBOHYD
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Matches
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A ZHU X., LING N., SHIMASAKI S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 190:1045-1052(1993).
C. -- FUNCTION: IGF-BINDING PROLEINS PROLONG THE HALF-LIFE OF THE IGFS
AND HAVE BEEN SHOWN TO ETHER INHIBIT OR STIMULATE THE GROWTH
PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
INTERACTION OF IGES WITH THEIRIT OR STIMULATE THE GROWTH
C. -- INSURE SPECIFICITY: MOSTLY IN KIDNEY.
C. -- SIMILARITY: TO OTHER INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS.
BRBL; LOB278; E7333; --
BRBL; A40403; A40403.
R PIR; A40403; F40403.
R PIR; F40403; F40403.
R PROSITE; PS00424; THYROGLOBULIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPEB_SCHPO STANDARD; PRT; 394 AA.
010088;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE AGMATINASE PRECURSOR (EC 3.5.3.11) (AGMATINE UREOHYDROLASE)
                                                                                                                                                                                                                                                                             POTENTIAL.
INSULIN-LIKE GROWTH FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 1; Length 271;
Pred. No. 4.48e+00;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                               THYROGLOBULIN TYPE I.
0AA79506 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTATIVE AGMATINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 1; LA
Pred. No. 4.48e+00;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0B0AFF49 CRC32;
                                                                                                                                                                                                                                                                                                                 PROTEIN 5.
                                                                                                                                                                                                                                                             GROWTH FACTOR BINDING; SIGNAL. SIGNAL 1 19 P CHAIN 20 271 I
                                                                                                                                                                                                                                                                                                                               214 262 T
271 AA; 30298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42879 MW;
                                                                                                                                                                                                                                                                                                                                                                                 Match 50.5%;
Local Similarity 41.7%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.5%;
Similarity 60.0%;
6; Conservative
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186
209
211
2113
307
                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 CRRHMEASLQEF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKRAMLAGLNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 RTTLSGLSDY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |:||:||
3 RAMLAGLNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAC11D3.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                             GASTROCNEMICS MUSCLE.
-!- SIMILARITY: TO OTHER INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS.
EMBL: 112447, 6293384; --
EMBL; 002025; 6437125; --
EMBL; 002023; 6437125; --
EMBL; 002024; 6437125; JOINED.
EMBL; 002024; 6437125; JOINED.
EMBL; 002024; 6437125; JOINED.
EMBL; 002024; 6437125; JOINED.
EMBL; 002024; G437125; JOINED.
PROSITE; PS00484; TEREJENDING; 1.
GROWTH FACTOR BINDING; SIGNAL.
                                                                                                                                                                                                                                                                             MOL. CELL. ENDOCRINOL. 104:57-66(1994).

-!- FUNCTION: IGF-BINDING PROTUEINS PROLONG THE HALF-LIFE OF THE IGFS
--- FUNCTION: IGF-BINDING PROTUEINS PROLONG THE HALF-LIFE OF THE IGFS
--- AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
INTERACTION OF IGFS WITH THEIR CELL CURFACE RECEPTORS.
--- SUBCELLULAR LOCATION: EXTRACELLULAR.
--- TISSUE SPECIFICITY: MOST ABUNDANI IN KIDNEY, UTERUS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                       MEDLINE; 94042976.
JAMES P.L., JONES S.B., BUSBY W.H. JR., CLEMMONS D.R., ROTWEIN P.;
J. BIOL. CHEM. 268:22305-22312(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
1NSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR (IGFBP-5)
1GFBP-5) (IGF-BINDING PROTEIN 5).
1GFBP5 OR IGFBP-5.
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 271 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5.
214 262 THYROGLOBULIN TYPE I.
112 112 MISSING (IN REF. 2).
271 AA; 30372 MW; 12DC64CA CRC32;
                                                                                                                        MEDLINE; 94307727.
KOU K., JENKINS N.A., GILBERT D.J., COPELAND N.G., ROTWEIN P.;
GENOMICS 20:412-418(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                            TISSUE-KIDNEY;
MEDLINE; 95121750.
SCHULLER A.G.P., GROFFEN C., VAN NECK J.W., ZWARTHOFF E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 271; Pred. No. 4.48e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-OVARY;
MEDLINE; 91244847.
SHIMASAKI S., SHIMONAKA M., ZHANG H.-P., LING N.;
J. BIOL. CHEM. 266:10646-10653(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 20-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
271
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STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 93176146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 CRRHMEASLQEF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| | |:| ::
1 CKRAMLAGLNDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; RODENTIA.
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                               SEQUENCE FROM N.A.
          TISSUE-MYOBLASTS;
                                                                                                            LISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT 14
IBP5_RAT
P24594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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Matches

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Gaps

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Length 271;

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Gaps

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1; Indels

Length 394;

Search completed: Fri Sep 25 13:14:37 1998 Job time : 8 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 8.32 Seconds 25.285 Million cell updates/sec Fri Sep 25 13:15:58 1998; Run on:

not generated Tabular output >PCT-US98-16719-16 (1-13) from PCTUS9816719A.pep 107 Title:

CKRAMLAGLNDYC 13 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

131922 seqs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq32 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 19.306; Variance 59.162; scale 0.326

tatistics:

SUMMARIES

Pred. No pAGDetail platelet apregation phototet aggregation phototet aggregation phototet aggregation phototet aggregation phototet aggregation platelet aggregation platelet aggregation platelet aggregation platelet aggregation platelet aggregation platelet aggregation phototet aggregation Echistatin fibrinogen Sequence of viper ven Platelet adhesion blo Description R12986 P91098 R42886 R42886 R42886 R42863 R46943 R46939 R42856 R42856 R42856 R42856 R42856 R42856 R42856 Length Query Score

5.64e+00 5.64e+00 5.64e+00 5.64e+00 7.23e+00 7.2
Trigramin-beta 1 Albolabrin peptide ta Albolabrin. Trigramin-beta 2. Disintegrin peptide # Disintegrin pinibito Diffunctional inhibito Diffunctional inhibito Diffunctional inhibito
R10109 W45500 R10106 R10106 R101106 R101106 R101103 R10113 R10113 R10113 R10113 R10113 R10113 R101013 R101013 R101013 R101013 R101013 R10103 R
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RESULT

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26-5EP-1991 (first entry)
Echistatin fibrinogen-receptor antogonist.
Fibrinogen: platelet; adhesion; bone; osteoclasts; aggregation.
Echis carinatus.
EP-437367-A.
 Š
R12986 standard; Protein; 49
                                                                                                  49 AA;
                                                                                                  Sequence
    R12986;
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Gaps ö 4; Indels Length 49; Score 68; DB 3; Le Pred. No. 2.66e+00; 1; Mismatches Query Match 63.6%; Best Local Similarity 61.5%; Matches 8; Conservative

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20 ckrargddlddyc 32 13 1 CKRAMLAGLNDYC 윱 à

13-MAR-1992 (first entry)
Sequence of viper venom polypeptide.
Platelet aggregation inihibtor; antithrombotic agent;
Myocardial infarction. ¥ LT 2 P91098 standard; Protein; 49 P91098; RESULT ID P99 AC P99 DT 13 DE SE KW P1

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05-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide composns. for blocking platelet adhesion to collagen - useful for e.g. preventing platelet thrombosis, thromboembolism useful for e.g. preventing platelet thrombosis, thromboembolism pr and re-occlusion during and after surgery
Salaim 1: Page 20; 21pp; English.

The sequences given in R24287-90 are peptides which are used in a method for inhibiting collagen-stimulated platelet activation that comprises blocking platelet adhesion to collagen by contacting with one of these peptides. The polypeptides are useful in surgery on peripheral arteries (arterial grafts, carotid endarterectomy) and in peripheral surgery to prevent the formation of thrombi and cardiovascular surgery to prevent the formation of thrombi and composemboli. They can also be used to prevent adhesion of Sequence 49 AA;
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                                                                                                                                                                                                                 viper venom polypeptide cpds. - useful in inhibiting platelet aggregation where strong antithrombotic activity of short duration is needed claim 13. Page 23; 33pp; English.

The polypeptides of the invention have been purified from the venom of various vipers, e.g. Trimeresurus gramineus, E.carinatus, Agkistrodon piscivorus, Bitis arietans and Eristocophis macmahonii. The polypeptides can be used to prevent platelet thrombosis, thromboembolism and reocclusion.
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Platelet adhesion blocking peptide (3).
Collagen-stimulated platelet activation; thrombi; thromboemboli.
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                25-OCT-1989.
17-APR-1989; 200967.
22-APR-1988; US-184653.
22-EBR-1989; US-303757.
01-FEB-1989; US-303757.
(MERI ) MERCK & CO INC.
Friedman PA, Polokoff MA, Gould RJ, Bencen GH, Jacobs JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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Pred. No. 3.42e+00;
2; Mismatches 4. Tandol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68; DB 4; Length 49; Pred. No. 2.66e+00;
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pAGbeta101 platelet aggregation inhibitory polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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R24289 standard; Protein; 49 AA.
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R42886 standard; Protein; 30 AA.
R42886;
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13-NOY-1991; 310449.
13-NOY-1990; US-612941.
27-FEB-1991; US-662225.
(MERI ) MERCK & CO INC.
CONDOLLY TW, KATCZEWSKI J;
WPI; 92-176837/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%;
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Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                  Garsky VM, Gan ZR;
WPI; 89-311082/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AA;
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EP-487238-A.
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Gaps
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                                                                                          03-0CT-1991; 256234.
26-0CT-1999; JP-287116.
20-FEB-1999; JP-287116.
20-FEB-1999; JP-287116.
WPI: 93-348481/44.
WPI: 93-348481/44.
WPISDB; Q50356.
Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
Example; Fig 2; 50pp; Japanese.
Example: Fig 2; 50pp; Japanese.
The sequence is that encoded by pAGbeta101 cDNA comprising a polypeptide isolated from Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypoptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example; Page 25; 50pp; Japanese.
The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid ar
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Platelet aggregation inhibitory peptide.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. 1975. 1994 (first entry) pAGbeta2-101 platelet aggregation inhibition; ADP; collagen; thrombin; arachidonic acid; PAF. Agkistrodon halys blomhoffi.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 8; Length 39;
Pred. No. 5.64e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 8; Length 30; Pred. No. 5.64e+00; 2; Mismatches 4; Indels
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R42853 standard; Protein; 39 AA.
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R46945 standard; Protein; 39 AA.
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26-0CT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 93-348481/44.
N-PSDB; Q44931.
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WPI; 93-348481/44.
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Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.7%;
Best Local Similarity 53.8%;
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26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
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7N J052332.
PD 05-OCT-1993;
PR 26-CT-1991; 256234.
PR 26-CT-1999; JP-287116.
PR 26-CT-1999; JP-287116.
PR 20-FEB-1991; JP-026328.
PR POLYPEPTIGE of specified aminoacid sequence - used for inhibiting PT platelet aggregation caused by e.g. collagen, thrombin, etc.
PR POLYPEPTIGE is that encoded by pAGDetal-101 cDNA comprising CC The sequence is that encoded by pAGDetal-101 cDNA comprising CC The sequence 39 AA;
Score 65; DB 8; Length 39;
Scouence 39 AA;
Score 65; DB 8; Length 39;
No. 5.64e+00;
A: Indels 0; Gap
                                                                                                                                                                                                                                                                                                                                                                                                               70 00-0CT-1991; 256334.
71 03-0CT-1991; 256334.
72 03-0CT-1991; 256334.
73 26-0CT-1991; DF-287116.
74 26-0CT-1991; JP-026328.
75 3-3484841/44.
76 WFI; 93-3484841/44.
76 PSDB: Q44924.
77 Polypeptide of specified aminoacid sequence - used for inhibiting PT platelet aggregation caused by e.g. collagen, thrombin, etc.
75 Example: Fig 4: 50pp; Japanese.
76 Example: Fig 4: 50pp; Japanese.
77 Collagence is that encoded by pAGbeta102 cDNA comprising CC a polypeptide isolated from Agkistrodon halys blomhoffi.
78 Sequence 39 AA;
                                                                                                                                                                                                                                           R46938;
11-MAY-1994 (first entry)
PAGDetal02 platelet aggregation inhibitory polypeptide.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1994 (first entry)
pAGbetal-101 platelet aggregation inhibitory polypeptide.
Inhibittion; ADP; collagen; thrombin; arachidonic acid; PAF.
JO5255395-A.
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Pred. No. 5.64e+00;
2; Mismatches 4.
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R42855 standard; Protein; 39 AA.
R42855;
11-MAY-1994 (first entry)
Platelet aggregation inhibitory peptide.
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R46938 standard; Protein; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                               crrargddlddyc 28
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1 CKRAMLAGLNDYC 13
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ID R4
AC R4
DT 11
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The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example; Fig 11; 50pp; Japanese.
The sequence is that encoded by pAGbeta2-101 cDNA comprising a polypeptide isolated from Agkistrodon halys blomhoffi.
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The sequence is that encoded by pAGbeta107 cDNA comprising a polypeptide isolated from Agkistrodon halys blomhoffi. Sequence 39 AA:
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ILMAY-1994 (first entry)
PAGBetalOY platelet aggregation inhibitory polypeptide.
Inhibition; ADP: collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1994 (first entry)
batelet aggregation inhibitory peptide.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
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Pred. No. 5.64e+00;
2; Mismatches 4; Indels
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Pred. No. 5.64e+00;
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Pred. No. 5.64e+00;
2; Mismatches 4; Indels
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R42851 standard; Protein; 39 AA.
R42851;
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R46943 standard; Protein; 39 AA.
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26-0CT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE ) TAKEDA CHEM IND LTD.
WPI; 93-348481/44.
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20-FEB-1991; JP-026328.
(TAKE ) TAKEDA CHEM IND LTD.
WPI; 93-348481/44.
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larity 53.8%;
Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Similarity 53.8%;
7; Conservative
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| CKRAMLAGINDYC 13
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                                                                                                                                                                                                      Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example: Page 26; 50pp; Japanese. The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example; Page 24; 50pp; Japanese. The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
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Platelet aggregation inhibitory peptide.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R42856 standard; Protein; 39 AA.
R42856;
11-MAY-1994 (first entry)
Platelet aggregation inhibitory peptide.
Inhibition; ABP; collagen; thrombin; arachidonic acid; PAF
Agkistrodon halys blomhoffi.
Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF. Agkistrodon halys blomhoffi.
J05255395-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 8; Length 39;
Pred. No. 5.64e+00;
2; Mismatches 4; Indels
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Pred. No. 5.64e+00;
2; Mismatches 4;
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03-OCT-1991; 256234.
26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI: 93-346481/44.
N-PSDB; Q50374.
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03-OCT-1991; 256234.
26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 93-348481/44.
N-PSDB; Q50379.
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03-OCT-1991; 256234.
26-OCT-1990; JP-287116.
20-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 93-348481/44.
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imilarity 53.8%;
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1 CKRAMLAGLNDYC 13
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| CKRAMLAGLNDYC 13
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atches 7; Conserv
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03-0CT-1991; 256234.
03-0CT-1990; JP-287116.
26-0CT-1990; JP-287116.
26-0CT-1990; JP-286328.
(TAKE ) TAKEDA CHEM IND LTD.
WPI; 93-34841/44.
POLYPEPTIGE of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
Example; Page 23; 50pp; Japanese.
The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc. Example: Page 26; 50pp: Japanese. The sequence is that of a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and
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26-0CT-1990; JP-287116.
26-0CT-1990; JP-287116.
WD-FEB-1991; JP-026328.
(TAKE) TAKEDA CHEM IND LTD.
WPI: 93-348481/44.
WPISDB; Q44925.
Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
Example; Fig 5; 50pp; Japanese.
Example; Fig 5; 50pp; Japanese.
The sequence is that encoded by pAGbeta103 cDNA comprising a polypeptide isolated from Agkistrodon halys blomhoffi.
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Asobetalo's platelet aggregation inhibitory polypeptide.
Inhibition; App. collagen: thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
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latelet aggregation inhibitory peptide.
Inhibition: ADP: collagen; thrombin; arachidonic acid; PAF.
Agkistrodon halys blomhoffi.
                                                                                                                                                                                                             Score 65; DB 8; Length 39; Pred. No. 5.64e+00; 2; Mismatches 4; Indels
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Pred. No. 5.64e+00;
2; Mismatches 4
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R42849 standard; Protein; 39 AA.
R42849;
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R46939 standard; Protein; 39 AA.
R46939;
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larity 53.8%;
Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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ö Best Local Similarity 53.8%; Pred. No. 5.64e+00; Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps

16 crrargddlddyc 28 |:|| |:||1 1 CKRAMLAGLNDYC 13

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Search completed: Fri Sep 25 13:16:08 1998 Job time : 10 secs.

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protein - protein database search, using Smith-Waterman algorithm ferch_pp

Fri Sep 25 13:15:28 1998; MasPar time 4.13 Seconds 114.891 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US98-16719-16 (1-13) from PCTUS9816719A.pep 107

1 CKRAMLAGLNDYC 13 Title: Description: Perfect Score: Sequence:

Scoring table:

120441 segs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 26.345; Variance 36.195; scale 0.728 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			•																				
Pred. No.	5.62e-02	1.41e-01	1.41e-01	1.41e-01	2.23e-01	2.23e - 01	2.23e-01	2.23e-01	5.46e-01	2.03e+00	3.12e+00	4.76e+00	4.76e+00	4.76e+00	4.76e+00	4.76e+00	4.76e+00	7.24e+00	1.09e+01	1.09e+01	1.09e+01	1.09e+01	1.09e+01
Description	fibrinolytic metallop	albolabrīn - green pi		trigramin beta-2 - In	echistatin alpha-2 -	echistatin (NMR, 8 st	echistatin alpha-1 -	echistatin beta - saw	E2 protein - human pa		L356 protein - Africa	hypothetical protein	CD40-associated prote	CD40 receptor-associa	INFR-associated prote	CD40 receptor-associa	artifact-warning sequ	hypothetical protein	L6 antigen - mouse	hypothetical protein	bel-1 protein - simia	bell protein - simian	hypothetical protein
Ü	JC4880	A23731	E35982	D35982	A35982	2ECH	A32029	S53431	WZWLE	F64498	A43680	H64533	I53498	I49272	A55649	A55960	D40201	S55612	A53399	C55514	WMLJS1	S18740	E64499
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& Query Match	62.6	60.7	60.7	60.7	59.8	59.8		59.8	57.9	55.1	54.2	53.3	53.3	53.3	53.3	53.3	53.3	52.3	51.4	51.4	51.4	51.4	51.4
Score	49	65	65	65	64	64	64	64	62	59	28	57	57	57	57	57	57	56	52	52	52	55	22
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Napier, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein IIb-IIIa protein antagonists from snake
venoms: evidence for a family of platelet-aggregation
inhibitors.
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#formal_name Trimeresurus gramineus #common_name Indian green
                                                                                                                                                                                                                                                                                                                                      #authors Calvete, J.J.; Schaefer, W.; Soszka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarowski, S. Jameson, Jameson
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#region cell attachment (R-G-D) motif\
#disulfide bonds #status experimental
#length 73 #molecular-weight 7573 #checksum 417
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Eur. J. Blochem. (1993) 218:853-860
(1)H*NR studies and secondary structure of the RGD-containing snake toxin, albolabrin.
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ACCESSIONS REFERENCE #authors #journal

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SUMMARY

Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.;
Napier, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein III-IIIa protein antagonists from snake venoms: evidence for a family of platelet-aggregation #formal_name Trimeresurus gramineus #common_name Indian green snake ö ö #type complete echistatin alpha-2 - saw-scaled viper #formal_name Echis carinatus #common_name saw-scaled viper 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change MA2\ #product trigramin beta-1 #status experimental #label *superfamily unassigned disintegrins; disintegrin homology *superfamily unassigned disintegrins; disintegrin homology *product trigramin beta-2 #status experimental #label Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napler, M.A.; Deisher, T.A.; Bunting, S.; Lazarus, R.A. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2471-2475
Platelet glycoprotein IIb-IIIa protein antagonists from si venoms: evidence for a family of platelet-aggregation Gaps Gaps tree viper
09-Nov-1990 #text_change #domain disintegrin homology (fragment) #label #length 73 #molecular-weight 7633 #checksum 534 ö ö 4; Indels Score 65; DB 2; Length 73; Pred. No. 1.41e-01; 2; Mismatches 4; Indels Length 73; D35982 #type complete trigramin beta-2 - Indian green tree viper trigramin beta-1 DB 2; Le 1.41e-01;

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##residues
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Polokoff, M.A.
#journal J. Biol. Chem. (1988) 263:19827-19832
#title Echistatin. A potent platelet aggregation inhibitor from the venom of the viper, Echis carinatus.
#cross-references MUID:89066819
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confidential alpha-1. saw-scaled viper
#formal_name Echis carinatus #common_name saw-scaled viper
07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
A32029; S29198
A32029; S29198
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2ECH #type complete

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GAGINSTATION (NMK, 8 structures) - saw-scaled viper

REFERENCE #formal_name Echis carinatus #common_name saw-scaled viper

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Biochemistry (1991) 30:7369
Three-dimensional structure of echistatin, the smallest
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#region turn (gamma' inverse turn)\
#region cell attachment (R-G-D) motif\
#region turn (gamma turn)\
#disulfide_bonds\
#disulfide_bonds\
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#disulfide_bonds\
#modified_site amidated carboxyl end (Thr)
#length 49 #molecular-weight 5425 #checksum 1074
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The secondary structure of echistatin from lh-NMR, circular-dichroism and raman spectroscopy.
length 47 #molecular-weight 5252 #checksum 3850
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Pred. No. 2.23e-01;
2; Mismatches 4; Indels
                                                       Length 47;
                                                    Score 64; DB 2; Le
Pred. No. 2.23e-01;
2; Mismatches 4;
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FEBS Lett. (1992) 309:316-320
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Resolution: not applicable
Determination: NMR
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llarity 53.8%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Chen, Y.L.; Huang, T.F.; Chen, S.W.; Tsai, I.H.
Biochem. J. (1995) 305:513-520
Determination of the structure of two novel echistatin
variants and comparison of the ability of echistatin
variants and comparison of the ability of echistatin
variants to inhibit aggregation of platelets from different
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#journal EMBO J. (1982) 1:231-236
#title Human papillomavirus la complete DNA sequence: a novel type of genome organization among papovaviridae.
#cross-references MUID:84182467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $53431  #type complete echistatin beta - saw-scaled viper #formal_name Echis carinatus #common_name saw-scaled viper 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                    ##molecule_type protein
##residues 1-21;25-49 ##label CAL
#Fresidues 1-21;25-49 ##label CAL
IFICATION #superfamily unassigned disintegrins; disintegrin homology
RDS disulfide bond; integrin inhibitor; venom
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#title The disulfide bridge pattern of snake venom disintegrins, flavoridin and echistatin. #cross-references WID:92387379 #accession S29198
                                                                                                                                                                                                                                                #domain disintegrin homology (fragment) #label DIS\
#region cell attachment (R-G-D) motif\
#disulfide_bonds #status predicted\
#disulfide_bonds #status experimental
#lasulfide_bonds #status experimental
#length 49 #molecular-weight 5425 #checksum 1074
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E2 protein - human papillomavirus type la
#formal_name human papillomavirus type la
18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change
16-Feb-1997
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#superfamily papillomavirus E2 protein
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Pred. No. 2.23e-01;
2; Mismatches 4;
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Pred. No. 2.23e-01;
2; Mismatches 4
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##molecule_type protein
##residues 1-50 ##label CHE
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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##molecule_type DNA
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#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
R.D.; Sutton, G.G.; Blake, J.A.; Flizocardú, L.M.; Clayton,
R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann,
J.L.; Nquyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson,
J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk,
H.P.; Fraser, C.M.; Smith, H.O.; Woose, C.R.; Venter, J.C.
#fournal Science (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon,
#toss.references.MUID:96337999
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L356 protein - African swine fever virus (strain BA71V)
#formal_name African swine fever virus, ASFV
28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change
09.5ep-1997
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                           selenium donor protein - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13.5ep-1996 #sequence_revision 13-5ep-1996 #text_change
10-oct-1997
DNA binding; early protein; transcription regulation #length 322 #molecular-weight 36923 #checksum 9041
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                                                                     Length 322;
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                                                                  Score 62; DB 1; Le
Pred. No. 5.46e-01;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                        #type complete
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#start_codon TTG
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##molecule_type DNA
                                                                Ouery Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conser
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*authors Action, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Glil, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Relley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.

#journal Nature (1997) 388:539-547
#title Helicobacter pylori.
#cross-references MUID:97394467
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#journal FEBS Lett. (1995) 358:113-118
#title A novel member of the TRAF family of putative signal
transducing proteins binds to the cytosolic domain of CD40.
#cross-references WulD:95129692
#accession I53498
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TIGR:HP0112
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hypothetical protein HP0112 - Helicobacter pylori (strain
26695)
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CD40-associated protein - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                            #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
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#length 231 #molecular-weight 27143 #checksum 4895
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##molecule_type mRNA
###readdocare
  Length 356;
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Pred. No. 4.76e+00;
1; Mismatches 5; Indels
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##cross-references GB:L38509; NID:g695357; PID:g695358
  DB 2; Le
3.12e+00;
                                                      6; Mismatches
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Score 58;
Pred. No.
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Matches 7: Constant
Query Match 54.2%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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                                                                                                         266 NRAMLISVKNFC 277
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Baltimore, D.
#journal Science (1995) 267:1494-1498
#title Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
#cross:references MUID:95184010
#accession 149272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E. Cell (1995) 80:389-399
The Epstein-Barr virus transforming protein LMPI engages signaling proteins for the tumor necrosis factor receptor
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W. H. M. M. J. O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
J. Biol. Cham. (1994) 269:30069-30072
A novel RING finger protein interacts with the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS649 #type complete
TNFR-associated protein LAPI - human
CD40-binding protein
#formal_name Homo sapiens #common_name man
13-3-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
AS5649; AS5135
                                                                                            Gaps
                                                                                                                                                                                                                                  149272 #type complete
CD40 receptor-associated factor 1 - mouse
#formal_name Mus musculus #common_name house mouse
15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
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CAP-1 #length 543 #molecular-weight 61719 #checksum 5192
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zinc finger
#length 567 #molecular-weight 64263 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residues 1-567 ##label RES
##cross-references EMBL:021050; NID:9719292; PID:9719293
                                                 Score 57; DB 2; Length 543;
Pred. No. 4.76e+00;
1; Mismatches 3; Indels
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##residues 1-133,135-404,'G',406-568 ##label HUA
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                 Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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149272
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1 CKRAMLAGINDYC 13
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##residues 1-56
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